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OM nucleic - nucleic search, using sw model

Run on: May 31, 2001, 06:37:45 ; Search time 1114.81 Seconds

(without alignments)
6191.188 Million cell updates/sec

Title: US-09-612-921-3

Perfect score: 468
Sequence: 1 atggtcctgagtgggcgct.....acttcacagcagtgactag 468

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1283235 segs, 7373929652 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
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2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
5: gb_in2:*
6: gb_in3:*
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95: gb_pr10:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	468	100.0	468	88 AF230377	AF230377 Homo sapi
2	468	100.0	1282	10 AX069307	AX069307 Sequence
3	468	100.0	1288	88 AF201830	AF201830 Homo sapi
4	468	100.0	2604	92 HSA242738	AJ242738 Homo sapi
5	468	100.0	2613	92 HSA242737	AJ242737 Homo sapi
6	468	100.0	2648	10 AX069309	AX069309 Sequence
7	468	100.0	2720	88 AF186094	AF186094 Homo sapi
8	351.2	75.0	468	10 AX069335	AX069335 Sequence
9	351.2	75.0	471	94 AF230378	AF230378 Mus muscu
10	351.2	75.0	1283	94 AF200495	AF200495 Mus muscu
11	351.2	75.0	1284	94 MMU250429	AJ250429 Mus muscu

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12 243 51.9 357 10 AX069304
13 243 51.9 985 10 AX069305
14 227 48.5 5751 10 AX069310
15 227 48.5 6540 92 HSA271338
16 227 48.5 7604 88 AF216693
17 227 48.5 7605 10 AX069311
18 227 48.5 198092 65 AC016724
19 174.2 37.2 8032 10 AX069334
20 110.8 23.7 998 9 AX048803
21 110.8 23.7 998 9 AX048805
22 110.2 23.5 462 9 ARI05636
23 110.2 23.5 474 9 A50276
24 110.2 23.5 474 9 AR001464
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26 110.2 23.5 474 9 AR085392
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28 110.2 23.5 531 9 A49726
29 110.2 23.5 531 9 A50144
30 110.2 23.5 534 93 HUMILRA
31 110.2 23.5 540 10 I09591
32 110.2 23.5 540 10 I09592
33 110.2 23.5 543 9 AR004317
34 110.2 23.5 578 92 HSL1LRAIT
35 110.2 23.5 579 9 A50279
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37 110.2 23.5 579 9 AR055510
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ALIGNMENTS

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AX069305 Sequence
AX069310 Sequence
AJ271338 Homo sapi
AF216693 Homo sapi
AX069311 Sequence
AC016724 Homo sapi
AX069334 Sequence
AX048803 Sequence
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ARI05636 Sequence
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A49726 Sequence 1
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I09592 Sequence 3
AR004317 Sequence
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AR001465 Sequence
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AR036273 Sequence
AR049621 Sequence
AR059551 Sequence
M55646 Human IcIL-
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RESULT 1
LOCUS AF230377 468 bp mRNA
DEFINITION Homo sapiens interleukin-1 delta mRNA, complete cds.
ACCESSION AF230377
VERSION AF230377.1 GI:9651788
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 468)
Debets, R., Timans, J.C., Zurawski, S., Sana, T.R., Bazan, F. and
Kastelein, R.A.
Novel IL-1 ligands IL-1d and IL-1e use IL-1R related protein 2
Unpublished
2 (bases 1 to 468)
Kastelein, R.A., Timans, J.C., Sana, T., Debets, R. and Bazan, F.
Direct Submission
JOURNAL Submitted (01-FEB-2000) Molecular Biology, DNAX Research Institute,
901 California Ave, Palo Alto, CA 94304, USA
FEATURES
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Best Local Similarity 100.0%; Pred. No. 8e-110;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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421 GGCTGGAATGCCCATCACAGACTTCTACTTCCAGAGTGTGACTAG 468
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RESULT 2
LOCUS AX069307 1282 bp DNA
DEFINITION Sequence 4 from Patent WO0102571.
ACCESSION AX069307
VERSION AX069307.1 GI:12579179
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1282)
Ford, J. and Pace, A.
A interleukin-1 receptor antagonist and uses thereof
Patent: WO 0102571-A 4 11-JAN-2001;
JOURNAL HXSEQ, INC. (US)
FEATURES
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BASE COUNT 294 a 337 c 350 g 301 t
ORIGIN
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73..540
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/db_xref="GI:6165336"
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2604
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698 a 579 c 656 g 671 t
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Best Local Similarity 100.0%; Pred. No. 6e-110;
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61 ctgataataacagctctctagctggaaggtctgcatgcaaggaagtcataaagtgaa 120
133 CTGATATAATACACAGCTTCTAGCTGAGGGGCTGCATGCGAAGAGCTATTAAGGTGAA 192
121 gagatcagcgtgtgtcccaatcgctgagtgagtgccagcgtctcccgcatctgtgt 180
193 GAGATCAGCGTGCTGCCAATCGGTGGTGGATGCGAGCTGTCCCGTCAATCCTGGGT 252
181 gtccaggtgtggaagcagctgtctgcatgtgtgtgtgtgtgtgtgtgtgtgtgtgt 240
253 GTCCAGGGTGAAGAGCAGTCCGTGCAATGTGGGTGGGCGAAGACCCAGCTTAAACATA 312
241 gagcagtgaaacatcatgagctctatctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 300
313 GAGCCAGTGAACATCATGAGCTTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 372
301 tacggcgaggacatgaggctcaccctcagctcagctcagctcagctcagctcagctc 360
373 TACGGCGGAGACATGAGGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAG 432
361 ctgtgcaagtgctcgtgaagcagctcagctcagctcagctcagctcagctcagctcag 420
433 CTGTGACAGGTGCTCGAAGCGCATCAGCCTGTCCACACTACCCAGCTTCCGAGATGAT 492
421 ggcgtgaatgcccccatcacagactctactctcagcagtgtagtag 468
493 GGCTGGAATGCCCCCATCAGACTTCTACTTCCAGCAGGTGTGACTAG 540

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JOURNAL
MEDLINE
20545212
REFERENCE
2 (bases 1 to 2613)
AUTHORS
Nicklin M.J.
TITLE
Direct Submission
JOURNAL
Submitted (09-JUN-1999) Nicklin M.J., Division of Molecular and
Genetic Medicine, University of Sheffield, Royal Hallamshire
Hospital, Glossop Road, Sheffield, S10 2UF, UNITED KINGDOM
FEATURES
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695 a 593 c 649 g 676 t
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Best Local Similarity 100.0%; Pred. No. 6e-110;
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502 GGCTGGAATGCCCCCATCAGACTTCTACTTCCAGCAGGTGTGACTAG 549

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RESULT 6
AX069309 2648 bp DNA PAT 25-JAN-2001
LOCUS AX069309
DEFINITION Sequence 6 from Patent WO0102571.
ACCESSION AX069309
VERSION AX069309.1 GI:12579181
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2648)
AUTHORS Ford, J. and Pace, A.
TITLE A Interleukin-1 receptor antagonist and uses thereof
JOURNAL Patent: WO 0102571-A 6 11-JAN-2001;
HYSEQ, INC. (US)
FEATURES
source Location/Qualifiers
1..2648
BASE COUNT 744 a 589 c 644 g 671 t
ORIGIN
Query Match 100.0%; Score 468; DB 10; Length 2648;
Best Local Similarity 100.0%; Pred. No. 6e-110;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 122 ctgcataataaacagctcttaagcttgagaggtcgaagaggaagtcattaaagtgaa 181
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DB 182 gagatcagcgtgtgtcccaatcggtgtgagatgcagcctgtcccgatcactcgtggt 241
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DB 482 ggcctggaatgcccccatcacaagacttacttccagcagtgtagactag 529

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LOCUS AF186094
DEFINITION Homo sapiens interleukin-1 receptor antagonist homolog (IL1HY1)
ACCESSION AF186094
VERSION AF186094.1 GI:6049804
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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REFERENCE 1 (bases 1 to 2720)
AUTHORS Mulero, J.J., Pace, A.M., Nelken, S.T., Loeb, D.B., Correa, T.R.,
Dranac, R. and Ford, J.E.
TITLE IL1HY1: A Novel Interleukin-1 Receptor Antagonist Gene
JOURNAL Biochem. Biophys. Res. Commun. 265 (3), 702-706 (1999)
PUBMED 10512743
REFERENCE 2 (bases 1 to 2720)
AUTHORS Mulero, J.J., Pace, A.M., Nelken, S.T., Loeb, D.B., Correa, T.R.,
Dranac, R. and Ford, J.E.
TITLE Direct Submission
JOURNAL Submitted (13-SEP-1999) Functional Genomics, HYSEQ Inc., 670
Almanor Ave., Sunnyvale, CA 94086, USA
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ORIGIN
Query Match 100.0%; Score 468; DB 88; Length 2720;
Best Local Similarity 100.0%; Pred. No. 6e-110;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 403 gagccagtgaaacatctgagctctatcttctgtgtccaaagaaatccaagagctcaccttc 462
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DB 463 taacggcggagaaatggtgtcctcactcagcttcagatcggtgtgctaccggggtgttc 522
QY 361 ctgtgacagtgctgtcctaaagcagctcagctgtgtcagactaacccaagctccggaatgtt 420
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QY 421 ggcctggaatgcccccatcacaagacttacttccagcagtgtagactag 468
DB 583 ggcctggaatgcccccatcacaagacttacttccagcagtgtagactag 630

RESULT 8
AX069335 468 bp DNA PAT 25-JAN-2001
LOCUS AX069335
DEFINITION Sequence 32 from Patent WO0102571.

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ACCESSION AX069335
 VERSION AX069335.1 GI:12579200
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 468)
 AUTHORS Ford J. and Pace A.
 TITLE A interleukin-1 receptor antagonist and uses thereof
 JOURNAL Patent: WO 0102571-A 32 11-JAN-2001;
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 Best Local Similarity 84.4%; Pred. No. 7.9e-80;
 Matches 395; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
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 Db 1 ATGGTTCTGAGTGGGGCACTATGCTTCGGAATGAGAGATTGCGCTTGAAGTACTGTAT 60
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 Oy 61 ctgcaataaaccagctctcagctgaagagctgcatgcaaggaaggtcaataaagtgaa 120
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 Db 61 CTGCACATTAACCACTGCTGCTGAGAGACTGCACGACGAGAGAAAGTCAATTAAGGTGAG 120
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 Oy 121 gagatcaagcgtgtgtcccaatcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 180
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 Db 121 GAGATCAAGTGTGTCCCAATCGGGCACTGGATGCGAGTGTGTCCCTGTCTATCTTG6GC 180
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 Oy 181 gtccagaggtggaagcagctgtcgtcatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 240
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 181 GTTCAAG 240
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 Oy 241 gagcagatgaacatcagctcagctctatctgtgtcgaaggaatcgaagctcagctc 300
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 Db 241 GAGCCAGTGAACATCATGAG 300
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 Oy 301 taccgggggagcataggggtcagctcagctcagctcagctcagctcagctcagctcagctc 360
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 Db 301 TACCGGGGAGATGAGTGTCTTACCTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 360
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 Oy 361 ctgtgcaagctgtcgtgaagcagctcagctcagctcagctcagctcagctcagctcagctc 420
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 Db 361 CTGTGCAAGCTTCAAGCAG 420
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 Oy 421 ggctggaatgcccccatcacagacttctacttcagcagtgtagtag 468
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 Db 421 GCCTGGAGTGTCTCCATCAGAGACTTCTTACAGAGAGTGTGACTAG 468
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 RESULT 9
 AF230378 471 bp mRNA ROD 02-AUG-2000
 LOCUS AF230378 Mus musculus Interleukin-1 delta mRNA, complete cds.
 DEFINITION AF230378
 ACCESSION AF230378.1 GI:9651790
 VERSION AF230378.1
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 471)
 AUTHORS Debets, R., Timans, J.C., Zurawski, S., Sana, T.R., Bazan, F. and Kastelein, R.A.
 TITLE Novel IL-1 ligands IL-1d and IL-1e use IL-1R related protein 2
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 471)
 AUTHORS Kastelein, R.A., Timans, J.C., Sana, T., Debets, R. and Bazan, F.
 TITLE Direct Submission
 JOURNAL Submitted (01-FEB-2000) Molecular Biology, DNAX Research Institute, 901 California Ave, Palo Alto, CA 94304, USA
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 source Location/Qualifiers
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 /protein_id="AA01275.1"
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 /translation="MMVLSGALCFRMKDSALVLYLHNNOLLAGLHAKEVITGEFIS
 VPRRALDASLSPYILVGSGSQGLSCGTGKGLIKLEPNIMELIYLAKESSTFTY
 RDMGLTSSFEASAYIPGMFLCTSPEDQPVRLTQIPEDPAMDAPITDFYFOCD"
 BASE COUNT 109 a 128 c 128 g 106 t
 ORIGIN
 Query Match 75.0%; Score 351.2; DB 94; Length 471;
 Best Local Similarity 84.4%; Pred. No. 7.9e-80;
 Matches 395; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
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 Db 4 ATGGTTCTGAGTGGGGCACTATGCTTCGGAATGAGAGATTGCGCTTGAAGTACTGTAT 63
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 Db 64 CTGCACATTAACCACTGCTGCTGAGAGACTGCACGACGAGAGAAAGTCAATTAAGGTGAG 123
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 Oy 121 gagatcaagcgtgtgtcccaatcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 180
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 Db 124 GAGATCAAGTGTGTCCCAATCGGGCACTGGATGCGAGTGTGTCCCTGTCTATCTTG6GC 183
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 Oy 181 gtccagaggtggaagcagctgtcgtcatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 240
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 Db 184 GTTCAAG 243
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 Oy 241 gagcagatgaacatcagctcagctctatctgtgtcgaaggaatcgaagctcagctc 300
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 Db 244 GAGCCAGTGAACATCATGAG 303
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 Oy 301 taccgggggagcataggggtcagctcagctcagctcagctcagctcagctcagctcagctc 360
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 Db 304 TACCGGGGAGATGAGTGTCTTACCTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 363
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 Oy 361 ctgtgcaagctgtcgtgaagcagctcagctcagctcagctcagctcagctcagctcagctc 420
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 Oy 421 ggctggaatgcccccatcacagacttctacttcagcagtgtagtag 468
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 Db 424 GCCTGGAGTGTCTCCATCAGAGACTTCTTACAGAGAGTGTGACTAG 471
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 RESULT 10
 AF200495 1283 bp mRNA ROD 11-MAY-2000
 LOCUS AF200495 Mus musculus Interleukin-1 homolog 3 mRNA, complete cds.
 DEFINITION AF200495
 ACCESSION AF200495
 VERSION AF200495.1
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1283)
 AUTHORS Kumar, S., McDonnell, P.C., Lehr, R., Tierney, L., Timans, M.N., Griswold, D.E., Capper, E.A., Tal-Singer, R., Wells, G.I., Doyle, M.L.

and Young, P.R.
Identification and initial characterization of four novel members
of the interleukin-1 family
J. Biol. Chem. 275 (14), 10308-10314 (2000)
JOURNAL MEDLINE 20209405
PUBMED 10744718
REFERENCE 2 (bases 1 to 1283)
AUTHORS Kumar, S., McDonnell, P.C. and Young, P.R.
TITLE Direct Submission
JOURNAL Submitted (01-NOV-1999) Bone and Cartilage Biology, UW 2109,
SmithKline Beecham Pharmaceuticals, 709 Swedeland Rd., King of
Prussia, PA 19406, USA

FEATURES

CDS

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/organism="Mus musculus"
/db_xref="taxon:10090"
/dev_stage="19.5 day embryo"
110..577
/note="cytokine; mIL-1H3; similar to Homo sapiens IL-1H3
sequence encoded by GenBank Accession Number AF186094"
/codon_start=1
/product="interleukin-1 homolog 3"
/protein_id="AA69251.1"
/db_xref="GI:7769118"
/translation="MWISGALCFRRKDSALVLYLHNNQLLAGLHAKEVYKGEISV
VPRNADSLSPVILGVGGSCSCGTEKPIILKEPVNIMELYLGAKESKSTFYR
RDMGTSFESAAYPGWFLCTSPADOPVRLTQIPEDPAMDAPITDFYFOCD"
BASE COUNT 325 a 317 c 309 g 332 t
ORIGIN

Query Match 75.0%; Score 351.2; DB 94; Length 1283;
Best Local Similarity 84.4%; Pred. No. 6.7e-80;
Matches 395; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 1 atggtctcgaatggtggcgctgtgtctccgaatgaagagctggcattgaagtcttat 60
DB 110 ATGGTCTCGAGTGGGGCACTATGCTCCGAATGAAGGATTCAGCCTTGAAGTACTGTAT 169
QY 61 ctgcataataaccagctcttagcttgaggtgcagatgcagaggaaggtcattaaagtgaa 120
DB 170 CTGCACAAATACACAGCTGCTGCTGGAGACCTGCACGCGAGAGAGTCAATTAAAGGTGAG 229
QY 121 gagatcagctgtgtcccaatcgctgtgcctgagatgcagcctgtcccgctcatcctgagt 180
DB 230 GAGATCAGTGTGTTGCCAATGCGGACATCGATGCCAGTCTGCCCTGTCAATCCTGGGCG 289
QY 181 gtccaggtgtgaagcagctgtgtcattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 240
DB 290 GTTCAAGGAGGAGGACGAGCTATCTTGTGGACAGAGAAAGGGCAATTCTGAACCTT 349
QY 241 gagccagtgaaatcatatgagctctatctgtgtccaagaatccaagaagcttacccttc 300
DB 350 GAGCCAGTGAATATCATGTAGAGCTTACTCTGGGGCCAAAGAAATCAAGAGCTTCACTTTC 409
QY 301 tacccgctggagacatgggtgtccacctccagcttcagatgcgtgtcctaccgggctgtgtc 360
DB 410 TACCGCGGGAGATATGGGTCTTACTCTCCAGCTTCGAATCCGCTACCCAGAGCTGTTC 469
QY 361 ctgtgcaaggtgtcctgtgaagcagatcagctgtcagatcaccagctcccgagaaagtgtc 420
DB 470 CTCTGCACCTTCACCGGAACCTGACCAGCTGTACAGCTTCACATCCCTGAGAGACCC 529
QY 421 ggcctgaatgccccatcacagacttacttaccagcaggtgtgagtag 468
DB 530 GCCTGGAGTCTCCATCACAGACTTCTACTTTCAGACAGTGTGACTAG 577

RESULT 11
LOCUS MMU250429 1284 bp mRNA
DEFINITION Mus musculus mRNA for IL-11l protein.
ACCESSION AJ250429

VERSION

AJ250429.1 GI:6165412
IL-11l protein.
house mouse.
Mus musculus

KEYWORDS

IL-11l protein.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 1284)
Barton, J.L., Herbst, R., Bosio, D., Higgins, L. and Nicklin, M.J.
A tissue specific IL-1 receptor antagonist homolog from the IL-1
cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities
Eur. J. Immunol. 30 (11), 3299-3308 (2000).

JOURNAL

20545212

MEDLINE

2 (bases 1 to 1284)

REFERENCE

Nicklin, M.J.H.

AUTHORS

Nicklin, M.J.H.

TITLE

Submitted (15-OCT-1999) Nicklin, M.J.H., Division of Molecular and
Genetic Medicine, University of Sheffield, S10 2UF, UNITED KINGDOM

JOURNAL

Hospital, Sheffield, S10 2UF, UNITED KINGDOM

COMMENT

Related sequence: A1391190.

FEATURES

Location/Qualifiers

source

1..1284
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/clone="IMAGE 332733"
113..580
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/db_xref="GI:6165413"
/db_xref="SPTREMBL:Q9QY11"
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BASE COUNT 327 a 317 c 310 g 330 t
ORIGIN

CDS

QY 1 atggtctcgaatggtggcgctgtgtctccgaatgaagagctggcattgaagtcttat 60
DB 113 ATGGTCTCGAGTGGGGCACTATGCTCCGAATGAAGGATTCAGCCTTGAAGTACTGTAT 172
QY 61 ctgcataataaccagctcttagcttgaggtgcagatgcagaggaaggtcattaaagtgaa 120
DB 173 CTGCACAAATACACAGCTGCTGCTGGAGACCTGCACGCGAGAGAGTCAATTAAAGGTGAG 232
QY 121 gagatcagctgtgtcccaatcgctgtgcctgagatgcagcctgtcccgctcatcctgagt 180
DB 233 GAGATCAGTGTGTTGCCAATGCGGACATCGATGCCAGTCTGCCCTGTCAATCCTGGGCG 292
QY 181 gtccaggtgtgaagcagctgtgtcattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 240
DB 293 GTTCAAGGAGGAGGACGAGCTATCTTGTGGACAGAGAAAGGGCAATTCTGAACCTT 352
QY 241 gagccagtgaaatcatatgagctctatctgtgtccaagaatccaagaagcttacccttc 300
DB 353 GAGCCAGTGAATATCATGTAGAGCTTACTCTGGGGCCAAAGAAATCAAGAGCTTCACTTTC 412
QY 301 tacccgctggagacatgggtgtccacctccagcttcagatgcgtgtcctaccgggctgtgtc 360
DB 413 TACCGCGGGAGATATGGGTCTTACTCTCCAGCTTCGAATCCGCTACCCAGAGCTGTTC 472
QY 361 ctgtgcaaggtgtcctgtgaagcagatcagctgtcagatcaccagctcccgagaaagtgtc 420
DB 473 CTCTGCACCTTCACCGGAAGCTGACCAGCTGTACAGCTTCACATCCCTGAGAGACCC 532
QY 421 ggcctgaatgccccatcacagacttacttaccagcaggtgtgagtag 468
DB 533 GCCTGGAGTCTCCATCACAGACTTCTACTTTCAGACAGTGTGACTAG 580

Query Match 75.0%; Score 351.2; DB 94; Length 1284;
Best Local Similarity 84.4%; Pred. No. 6.7e-80;
Matches 395; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

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Matches 243; Conservative	0; Mismatches 0;	Indels 0;	Gaps 0;	
OY	226 ccgactctaaacctaagaccagttaacatcataggagcgtctattctgtgtccaaagaatccc	285		
Db	1 ccgaccttttACACTGTAGAGCAGTAGATCATATGAGAGCTTATTCTTGTTGCCAAGGAATCC	60		
OY	286 aagagcttcaaccttataccgcggcggaacalbgggctcacctccagcttcgagtcgctgcc	345		
Db	61 AAGAGCTTCACCTCTTACC GGCGGGACAATGGGGCTCACCTCCAGCTTGAGTGGGCTGCC	120		
OY	346 taaccgggcttggttccctgtgtcaagygltgcctgaagccgatccagctctgaagatcccca	405		
Db	121 TACCCGGGCTGGTCTCTCTGTGCACGGGTGCCTGAAGCGATCAGCCTGTGAGACTCACCCAG	180		
OY	406 ctctcccgagaatggtgtgcgtggaatcccccatcacagagcttacttccagcagtgtagc	465		
Db	181 CTTCCCGAGAATGGTGGCTGGAAATGCCCAATCCCAATCAGACTTCTACTTCAGAGTGTGAC	240		
OY	466 tag 468			
Db	241 TAG 243			
RESULT 14				
LOCUS	AX069310	5751 bp	DNA	PAT 25-JAN-2001
DEFINITION	Sequence 7 from Patent WO0102571.			
ACCESSION	AX069310			
VERSION	AX069310.1	GI:12579182		
KEYWORDS	.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE	1 (bases 1 to 5751)			
AUTHORS	Ford,J., and Pace,A.			
TITLE	A interleukin-1 receptor antagonist and uses thereof			
JOURNAL	Patent: WO 0102571-A 7 11-JAN-2001;			
FEATURES	HYSEQ, INC. (US)			
source	Location/Qualifiers			
	1..5751			
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BASE COUNT	1466 a	1274 c	1489 g	1383 t
ORIGIN				139 others
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Best Local Similarity	100.0%; Pred. No. 4.1e-48;			
Matches 227; Conservative	0; Mismatches 0;	Indels 0;	Gaps 0;	
OY	242 agccagtgacaatcatatgagctctatatcttgtgtccaaagaatccaagagcttcaactctc	301		
Db	4073 ACCCAGTGTAACTATGTAGGCTCTATCTTGTGGCCAAGGAATCCAAGAGCTTCACCTTCT	4132		
OY	302 accgcgcggaactgtgggtcacctccagcttcgaatgctgtcctaccgcggctgtgtcc	361		
Db	4133 ACCGGCGGACACTGGGGCTCACTCCAGCTTGGAATCGGCTGCCAATCCCGGGCTGGTCC	4192		
OY	362 tgttcagtgctcgttaaagccgatacagctctgttcagataccaacagcttcccgagaatgtg	421		

Db 4193 TGTGACGCTGCTGATGACCGATCCTGTCTGACTCACCAGCTTCCCGAATGTTG 4252
QY 422 gctggaatgccccatcacagacttacttccagcagtgtactag 468
Db 4253 GCTGGATGCCCCCATCACAGACTTCTACTTCAGCAGTGTGACTAG 4299

RESULT 15
HSA271338 6540 bp DNA PRI 02-NOV-2000
LOCUS HSA271338
DEFINITION Homo sapiens IL1L1 gene for interleukin-1 like protein 1, exons 1-6.
ACCESSION AJ271338
VERSION AJ271338.1 GI:6729586
KEYWORDS IL1L1 gene; interleukin-1 like protein 1.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Barton, J.L., Herbst, R., Bostisio, D., Higgins, L. and Nicklin, M.J. A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities Eur. J. Immunol. 30 (11), 3299-3308 (2000)
JOURNAL 20345212
MEDLINE 2 (bases 1 to 6540)
REFERENCE Nicklin, M.J.H.
AUTHORS Direct Submission
TITLE Submitted (17-JAN-2000) Nicklin M.J.H., Division of Molecular and Genetic Medicine, University of Sheffield, Royal Hallamshire Hospital, Sheffield, South Yorkshire, UNITED KINGDOM
JOURNAL Location/Qualifiers
FEATURES
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2631..2716
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2717..3904
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4234..6522
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/number="6"
BASE COUNT 1747 a 1458 c 1709 g 1626 t
ORIGIN

Query Match 48.5%; Score 227; DB 92; Length 6540;
Best Local Similarity 100.0%; Pred. No. 4e-48;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 agccagtgacacatcatctgagctctatcttgytgcgaaggaatccaagaagcttcaccttct 301
Db 4232 AGCCAGTGAACATCATGAGCTCTATCTTGTCAGGAATCCAGAGCTTCACCTTCT 4291
QY 302 accgycggagacatggggctcacctcagcttcgagtcggtcctacccgggctggttc 361
Db 4292 ACCGGGGGACATGGGGCTCACCTCAGCTTGAGTGGGCTGCTACCCGGGCTGTTCC 4351
QY 362 tgtgcaagtgctcgaagcgcgatacagctcgtctagagctcaaccagcttcggagaatgtg 421
Db 4352 TGTGACGCTGCTGATGAGCCGATCAGCTGTCAGACTCACCAGCTTCCCGAATGTTG 4411
QY 422 gctggaatgccccatcacagacttacttccagcagtgtactag 468
Db 4412 GCTGGATGCCCCCATCACAGACTTCTACTTCAGCAGTGTGACTAG 4458

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Job time: 5877 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2001, 07:36:51 ; Search time 127.02 Seconds

(without alignments)
2150.918 Million cell updates/sec

Title: US-09-612-921-3

Perfect score: 468
Sequence: 1 atggctcgtgagtgaggcgcct.....actccagcagtgactag 468

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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- 5: /SID56/gcgdata/geneseq/geneseqn/NA1984.DAT:*
- 6: /SID56/gcgdata/geneseq/geneseqn/NA1985.DAT:*
- 7: /SID56/gcgdata/geneseq/geneseqn/NA1986.DAT:*
- 8: /SID56/gcgdata/geneseq/geneseqn/NA1987.DAT:*
- 9: /SID56/gcgdata/geneseq/geneseqn/NA1988.DAT:*
- 10: /SID56/gcgdata/geneseq/geneseqn/NA1989.DAT:*
- 11: /SID56/gcgdata/geneseq/geneseqn/NA1990.DAT:*
- 12: /SID56/gcgdata/geneseq/geneseqn/NA1991.DAT:*
- 13: /SID56/gcgdata/geneseq/geneseqn/NA1992.DAT:*
- 14: /SID56/gcgdata/geneseq/geneseqn/NA1993.DAT:*
- 15: /SID56/gcgdata/geneseq/geneseqn/NA1994.DAT:*
- 16: /SID56/gcgdata/geneseq/geneseqn/NA1995.DAT:*
- 17: /SID56/gcgdata/geneseq/geneseqn/NA1996.DAT:*
- 18: /SID56/gcgdata/geneseq/geneseqn/NA1997.DAT:*
- 19: /SID56/gcgdata/geneseq/geneseqn/NA1998.DAT:*
- 20: /SID56/gcgdata/geneseq/geneseqn/NA1999.DAT:*
- 21: /SID56/gcgdata/geneseq/geneseqn/NA2000.DAT:*
- 22: /SID56/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	468	100.0	468	20	X89432 Human interleukin
2	468	100.0	468	21	A51597 Human IL-1 receptor
3	468	100.0	766	21	A09193 Human IL-1 homolog
4	468	100.0	1282	20	Z30050 cDNA encoding a hu
5	468	100.0	1323	21	Z50812 Human TANGO-93 CDN
6	468	100.0	2490	21	Z50813 Human TANGO-93 CDN
7	468	100.0	2648	20	Z30051 cDNA encoding a hu
8	351.2	75.0	468	22	C81700 Murine interleukin
9	351.2	75.0	1275	21	A09198 Murine IL-1 homolo
10	351.2	75.0	1360	21	Z50811 Murine TANGO-93 CD
11	351.2	75.0	1385	21	A51599 Murine IL-1 recept

12	350.2	74.8	470	19	V71958
13	348.2	74.4	468	20	X89431
14	330.8	70.7	465	21	A09194
15	328	70.1	465	21	A09195
16	243	51.9	358	20	Z30048
17	241.4	51.6	985	20	Z30049
18	236	50.4	295	21	A51598
19	227	48.5	5752	20	Z30053
20	227	48.5	7605	20	A51600
21	208.6	44.6	382	21	Z35256
22	111.8	23.9	531	17	T33177
23	111.8	23.9	531	17	T30158
24	111.8	23.9	531	17	T30158
25	111.8	23.9	557	16	O89792
26	110.8	23.7	998	22	A89175
27	110.2	23.5	456	14	O40754
28	110.2	23.5	462	18	T38808
29	110.2	23.5	462	19	V36455
30	110.2	23.5	514	16	O83763
31	110.2	23.5	514	18	T72210
32	110.2	23.5	514	20	X82158
33	110.2	23.5	531	17	T35255
34	110.2	23.5	531	17	T30157
35	110.2	23.5	531	17	T30159
36	110.2	23.5	532	12	O14693
37	110.2	23.5	540	10	N92441
38	110.2	23.5	543	19	V22666
39	110.2	23.5	577	20	Z09793
40	110.2	23.5	578	20	Z09794
41	110.2	23.5	579	17	T15099
42	110.2	23.5	589	16	O90813
43	110.2	23.5	600	10	N92443
44	110.2	23.5	600	14	O40753
45	110.2	23.5	602	19	V65260

ALIGNMENTS

RESULT 1	
X89432	
ID	X89432 standard; DNA; 468 BP.
XX	
AC	X89432;
XX	
DT	28-SEP-1999 (first entry)
XX	
DE	Human interleukin 1 delta encoding DNA.
XX	
KW	interleukin 1 delta; IL-1 delta; glaucoma; ectodermal dysplasia;
KW	insulin-dependent diabetes mellitus; wrinkly skin syndrome;
KW	T-cell leukemia; lymphoma; tibial muscular dystrophy; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	1..468
FT	/tag= a
FT	/product= "IL-1 delta"
XX	
PN	W09935268-A1.
XX	
PD	15-JUL-1999.
XX	
PF	08-JAN-1999; 99WO-US00514.
XX	
PR	01-JUN-1998; 98US-0087393.
XX	
PR	09-JAN-1998; 98US-0071074.
XX	
PA	(IMMV) IMMUNEX CORP.
XX	
PI	Sims, JE.
XX	

Rodent interleukin
Mouse interleukin
Human IL-1 homolog
Human IL-1 homolog
cDNA encoding a hu
cDNA encoding a hu
Human IL-1 recepto
DNA encoding a hum
Murine IL-1 recept
Human interleukin-
Human interleukin-
Interleukin-1 rece
IL-1ra gene. Homo
Human interleukin-
IL-1 inhibitor (IL
Recombinant human
Recombinant human
Plasmid 15424. Sy
DNA encoding leade
Leaderless IL-1 re
Human interleukin-
Interleukin-1 rece
Interleukin-1 rece
IRAP gene. Homo s
Sequence of bps 61
cDNA encoding an I
IRAP conserved DNA
ICIRAP conserved D
Intracellular IL-1
Human IL-1 recepto
Sequence of GT10-1
GT10-IL-11-2A frag
Human intracellular

DR WPI: 1999-458310/38.
DR P-PSDB: Y28408.

PT Murine and Human interleukin 1 delta DNA, polypeptides and its
XX fragments, useful as molecular weight markers

PS Claim 1; Page 68; 72pp; English.

XX The present sequence encodes human interleukin 1 delta (IL-1 delta).
CC IL-1 delta proteins are useful for the determination of the molecular
CC weight of a sample protein. The protein and its fragments are useful as
CC controls for peptide fragmentation. This is useful for determining the
CC isoelectric point of a sample protein. Antibodies generated against
CC IL-1 delta and its fragmented peptides can be used to enhance the
CC accuracy of these molecular weight markers to determine the apparent
CC molecular weight and isoelectric point of a sample protein. IL-1 delta
CC can be used to screen for potential inhibitors of activity associated
CC with IL-1 delta counter-structure molecules. IL-1 delta can also be used
CC as therapeutic agents for the treatment of diseases mediated by IL-1
CC delta. IL-1 delta may be used as a reagent in studying the interleukin 1
CC (IL-1) signalling pathway, or as a reagent to block IL-1 signalling. The
CC IL-1 delta coding sequences can be used to identify human chromosome 2,
CC and to identify genes associated with certain diseases, especially with
CC region 2q11-12, including glaucoma, ectodermal dysplasia, insulin-
CC dependent diabetes mellitus, wrinkle skin syndrome, T-cell leukemia/
CC lymphoma and tibial muscular dystrophy.

XX Sequence 468 BP; 95 A; 128 C; 142 G; 103 T; 0 other;

Query Match 100.0%; Score 468; DB 20; Length 468;
Best Local Similarity 100.0%; Pred. No. 3,4e-127;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atgtgccgagtgaggcgctgtgtcgcgaatgaagagctcgcagtgatgctttat 60
DB 1 atgtgccgagtgaggcgctgtgtcgcgaatgaagagctcgcagtgatgctttat 60
OY 61 ctgtcataaaccagctctcagctgagagctgcatgacgaggaagtcattaaagtga 120
DB 61 ctgtcataaaccagctctcagctgagagctgcatgacgaggaagtcattaaagtga 120
OY 121 gagatcagcgtgtgtcccaatcgtgtgagtgccagcctgtcccgctcatcctgg 180
DB 121 gagatcagcgtgtgtcccaatcgtgtgagtgccagcctgtcccgctcatcctgg 180
OY 181 gtccagagtgtaagcagctgtcctgtcagtggtgggagcaggaacgacttaacata 240
DB 181 gtccagagtgtaagcagctgtcctgtcagtggtgggagcaggaacgacttaacata 240
OY 241 gaggcagtgaaacatcatgagctctatctgtgtgccaaggaatccaaagcttccttc 300
DB 241 gaggcagtgaaacatcatgagctctatctgtgtgccaaggaatccaaagcttccttc 300
OY 301 taccggcgagacatgaggctcaccctcagctcagctcgtcgtacccggcgctgttc 360
DB 301 taccggcgagacatgaggctcaccctcagctcagctcgtcgtacccggcgctgttc 360
OY 361 ctgtgtcagcgtgtcgtcgaagcagatcagcctgtcagactcaccagctccgagaatgt 420
DB 361 ctgtgtcagcgtgtcgtcgaagcagatcagcctgtcagactcaccagctccgagaatgt 420
OY 421 ggcctgaatgcccccatcacagactctacttcacagcagtgatgata 468
DB 421 ggcctgaatgcccccatcacagactctacttcacagcagtgatgata 468

RESULT 2
ID A51597
XX A51597 standard; DNA: 468 BP.
AC A51597;
XX

DT 31-Oct-2000 (first entry)
XX
DE Human IL-1 receptor antagonist 3 DNA.
XX

KW hIL-1ra3; human interleukin-1 receptor antagonist-3; IL-1lp; osteopathic;
KW interleukin-1-like polypeptide; anti-inflammatory; anti-asthmatic;
KW anti-arthritis; antimicrobial; respiratory; anti-ischemic; vaccine;
KW dermatological; immunomodulatory; gastrointestinal; gene therapy; ds.
XX

OS Homo sapiens.

XX Key Location/Qualifiers
FT CDS 1..468
FT /tag= a
FT /product= hIL-1ra3

XX MO200039297-A2.

XX 06-JUL-2000.

XX 22-DEC-1999; 99WO-US30720.

XX 23-DEC-1998; 98US-0113430.

XX 22-JAN-1999; 99US-0116843.

XX 13-APR-1999; 99US-0129122.

XX (GETH) GENENTECH INC.

XX Goddard A. Pan J;

XX WPI: 2000-452395/39.

XX P-PSDB: Y96936.

XX Nucleic acids encoding interleukin-1-like polypeptides, useful for
XX preventing and treating e.g. inflammation, asthma and psoriasis
XX Claim 7; Fig 7; 143pp; English.

XX An isolated nucleic acid molecule encoding an interleukin-1-like
XX polypeptide (IL-1lp) that retains one or more activities of the peptide
XX from which it is derived, such as the IL-18R binding activity of a human
XX interleukin-1 receptor antagonist-1 (hIL-1Ra1) polypeptide, is new. The
XX nucleic acids may be used in molecular engineering applications, e.g.
XX hybridization assays and chromosome and gene mapping studies, for
XX recombinantly producing the IL-1lp polypeptide or for producing gene
XX knock out animals to study the role of the protein in metabolism and
XX disease processes (conversely, gene therapy protocols may be used to
XX supplement a patient's production of the polypeptide or to rectify
XX mutations that lead to the production of in active peptides). The
XX peptides produced may be used to screen for and produce modulators (e.g.
XX antibodies) of IL-1lp protein expression and activity which may be use
XX to treat disorders associated with inappropriate IL-1lp expression and
XX activity, such as inflammatory disorders, asthma, arthritis,
XX osteoarthritis, sepsis, acute lung injury, adult respiratory distress
XX syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
XX psoriasis, graft versus host disease and/or inflammatory bowel disease.

XX Sequence 468 BP; 95 A; 128 C; 142 G; 103 T; 0 other;

Query Match 100.0%; Score 468; DB 21; Length 468;
Best Local Similarity 100.0%; Pred. No. 3,4e-127;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atgttcctgagtgaggcgctgtgtcctcgaatgaagagctcgcagtgatgctttat 60
DB 1 atgttcctgagtgaggcgctgtgtcctcgaatgaagagctcgcagtgatgctttat 60
OY 61 ctgtcataaaccagctctcagctgagagctgcatgacgaggaagtcattaaagtga 120
DB 61 ctgtcataaaccagctctcagctgagagctgcatgacgaggaagtcattaaagtga 120
OY 121 gagatcagcgtgtgtcccaatcgtgtgagtgccagcctgtcccgctcatcctgg 180

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Db      121 gagatcagcgtggtccccaatcgctgctgagatgcagcctgtcccccgtcatccgggt 180
Oy      181 gtcccaagggtgaagcagcagctgctgctgagtgaggcaggagccgacttaacacta 240
Db      181 gtcccaagggtgaagcagcagctgctgctgagtgaggcaggagccgacttaacacta 240
Oy      241 gagccagtgacaatcatctgagctctactctgtgtccaaagaaatcaagagctcacctc 300
Db      241 gagccagtgacaatcatctgagctctactctgtgtgtccaaagaaatcaagagctcacctc 300
Oy      301 tacccggcgagaaatgagtgctcacctccagcttcagtcgagtcgactaccggcgctgttc 360
Db      301 tacccggcgagaaatgagtgctcacctccagcttcagtcgagtcgactaccggcgctgttc 360
Oy      361 ctgtgacagctgctcctgaagccgatacagctgtgacagcttaccagctcccgagatgt 420
Db      361 ctgtgacagctgctcctgaagccgatacagctgtgacagcttaccagctcccgagatgt 420
Oy      421 ggcctggaatgcccccatcacagactctactctcagcagtgtagctag 468
Db      421 ggcctggaatgcccccatcacagactctactctcagcagtgtagctag 468

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RESULT 3
A09193 ID A09193 standard; DNA; 766 BP.
AC A09193:
DT 10-AUG-2000 (first entry)
DE Human IL-1 homologue, hzllia3 coding sequence.
KM Generic: interleukin-1; IL-1; homologue; zllia3; anti-inflammatory;
KM antagonistic; pro-inflammatory; agonist; immunomodulator; antiarthritic;
KM antirheumatic; osteoporotic; antipsoriatic; antibacterial; cytostatic;
KM immunosuppressive; antidiabetic; antidiabetic; nephrotropic; vasotropic;
KM vulnerability; 2q14; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 72..539
FT /tag= a
FT PN MO200020595-A1.
PD 13-APR-2000.
XX 08-OCT-1999; 99WO-US23533.
XX 08-OCT-1998; 98US-0169745.
XX 08-OCT-1998; 98US-0169745.
XX (ZYMO ) ZYMOGENETICS INC.
XX Sheppard PO, West RR, Clegg CH;
XX WPI: 2000-303780/26.
XX P-PSDB: Y92257.
XX
XX Proteins useful for treatment of inflammatory conditions such as
XX Rheumatoid arthritis and psoriasis are agonists or antagonists forms of
XX new interleukin-1 homologue
XX
XX Disclosure: Page 51-52; 64pp; English.
XX
XX This DNA encodes an interleukin-1 (IL-1) homologue, designated zllia3.
XX The zllia3 gene maps to chromosome 2q14 and showed linkage to framework
XX marker AFM037xfl with a LOD score of 13.
XX It is believed that zllia3 acts through IL-1 receptors. In general,
XX zllia3 proteins having a Lys residue at position 148 will have
XX anti-inflammatory activity (e.g. Y92256), whilst those having Asp

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CC (see Y92254) or Glu at this position will have pro-inflammatory action.
CC zllia3 is used to modulate an immune response in an animal (claimed).
CC Antagonists zllia3 forms may be used to treat or prevent chronic
CC inflammatory diseases such as rheumatoid arthritis, osteoarthritis and
CC Lyme arthritis, psoriasis, to reduce tissue damage after ischemia, to
CC treat septic shock, graft-versus-host disease and leukemia.
CC The antagonists may also alleviate inflammatory bowel disease including
CC Crohn's disease and ulcerative colitis, insulin-dependent diabetes
CC mellitus, acute pancreatitis, glomerulonephritis and cerebral ischemia.
CC Agonist forms of zllia3 may promote wound healing by IL-1 effects on
CC growth factor secretion and cell proliferation. They may also treat
CC infections, especially gastrointestinal infections.
XX
XX SQ Sequence 766 BP; 154 A; 214 C; 230 G; 168 T; 0 other;

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Query Match 100.0%; Score 468; DB 21; Length 766;
Best Local Similarity 100.0%; Pred. No. 4,1e-127;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy      1 atggtctcagtgaggcgctgtgcttcggaatgaagagctcgcatgaggtgctttat 60
Db      72 atggtctcagtgaggcgctgtgcttcggaatgaagagctcgcatgaggtgctttat 131
Oy      61 ctgcataataaccagctctagctggaaggctgcatgacaggaaggtcataaaggtgaa 120
Db      132 ctgcataataaccagctctagctggaaggctgcatgacaggaaggtcataaaggtgaa 191
Oy      121 gagatcagcgtgtgtcccaatcggtgtgctgagtcgacgctgtcccgctatcctggt 180
Db      192 gagatcagcgtgtgtcccaatcggtgtgctgagtcgacgctgtcccgctatcctggt 251
Oy      181 gtcccaagggtgaagccagctgctgcatgtgggtgtggcagaagccgacttaacacta 240
Db      252 gtcccaagggtgaagccagctgctgcatgtgggtgtggcagaagccgacttaacacta 311
Oy      241 gagccagtgacaatcatctgagctctactctgtgtgccaagaaatccaaagctcacctc 300
Db      312 gagccagtgacaatcatctgagctctactctgtgtgtgccaagaaatccaaagctcacctc 371
Oy      301 tacccggcgagaaatgagtgctcacctccagcttcagtcgagtcgactaccggcgctgttc 360
Db      372 tacccggcgagaaatgagtgctcacctccagcttcagtcgagtcgactaccggcgctgttc 431
Oy      361 ctgtgacagctgctcctgaagccgatacagctgtgacagcttaccagctcccgagatgt 420
Db      432 ctgtgacagctgctcctgaagccgatacagctgtgacagcttaccagctcccgagatgt 491
Oy      421 ggcctggaatgcccccatcacagactctactctcagcagtgtagctag 468
Db      492 ggcctggaatgcccccatcacagactctactctcagcagtgtagctag 539

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RESULT 4
Z30050 ID Z30050 standard; cDNA; 1282 BP.
AC Z30050:
DT 26-JAN-2000 (first entry)
DE cDNA encoding a human Interleukin-1 receptor antagonist.
XX
XX Human; interleukin-1 receptor; IL-1; antagonist; sepsis;
XX acute pancreatitis; endotoxic shock; cytokine induced shock;
XX Rheumatoid arthritis; chronic inflammatory arthritis;
XX pancreatic cell damage; diabetes mellitus type 1;
XX graft versus host disease; inflammatory bowel disease;
XX inflammation; pulmonary disease; autoimmune disease;
XX inflammatory disease; antiproliferative; myelogenous leukemia;
XX premature labor; intrauterine infection; nutritional activity;
XX hematopoiesis regulating activity; tissue growth activity;
XX activin activity; inhibin activity; chemotactic activity;

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KW chemokine activity; hemostatic activity; thrombolytic activity;
 KW anti-inflammatory activity; ss.
 OS Homo sapiens.
 PN W09951744-A2.
 XX 14-OCT-1999.
 PD 14-OCT-1999.
 XX 05-APR-1999; 99WO-US04291.
 XX 03-APR-1998; 98US-0055010.
 PR 15-MAY-1998; 98US-0079909.
 PR 20-MAY-1998; 98US-0082364.
 PR 19-JUN-1998; 98US-0099818.
 PR 31-JUL-1998; 98US-0127698.
 PR 13-JAN-1999; 99US-0229591.
 PR 17-FEB-1999; 99US-0251370.
 XX (HYSE-) HYSEQ INC.
 PA Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
 PI Leshkowitz D, Kita D, Ford J, Pace A, Alfemito M;
 XX WPI: 1999-611042/52.
 DR P-PSDB; Y43526.
 XX New isolated interleukin-1 receptor binding polypeptides, used to treat
 PT e.g. sepsis, shock, arthritis, pancreatitis, graft-versus-host disease,
 PT inflammatory disease, autoimmune disease or proliferative disease -
 PS Claim 1, Fig 5; 123pp; English.
 XX The present sequence encodes a human interleukin-1 (IL-1) receptor
 CC antagonist. The encoded polypeptide is capable of binding IL-1
 CC receptors (IL-1Rs). The polynucleotides and polypeptides can be used for
 CC the prevention or treatment of disorders involving sepsis, acute
 CC pancreatitis, endotoxic shock, cytokine induced shock, rheumatoid
 CC arthritis, chronic inflammatory arthritis, pancreatic cell damage from
 CC diabetes mellitus type 1, graft versus host disease, inflammatory bowel
 CC disease, inflammation associated with pulmonary disease, other autoimmune
 CC disease or inflammatory disease, an antiproliferative agent such as for
 CC acute or chronic myelogenous leukemia or in the prevention of premature
 CC labor secondary to intrauterine infections. They can also exhibit
 CC activities such as e.g. nutritional activity, cytokine and cell
 CC proliferation/differentiation activity, immune stimulating or
 CC suppressing activity, hematopoiesis regulating activity, tissue growth
 CC activity, activin/inhibin activity, chemotactic/chemokinetic activity,
 CC hemostatic and thrombolytic activity, receptor/ligand activity, and
 CC anti-inflammatory activity. The products can also be used for
 CC detection, diagnosis and drug screening.
 XX Sequence 1282 BP; 293 A; 337 C; 350 G; 301 T; 1 other:
 SQ

Query Match 100.0%; Score 468; DB 20; Length 1282;
 Best Local Similarity 100.0%; Pred. No. 5e-127;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgtcctcgtatggtggcgctgtcttcgaaagaaagcctggactggaagtgtcttat 60
 |||||||
 DB 73 atgtcctcgtatggtggcgctgtcttcgaaagaaagcctggactggaagtgtcttat 132
 |||||||
 QY 61 ctgtcataataaccagctcttagcttggaaggtcgtcatgcaaggaaagtcattaaagttaa 120
 |||||||
 DB 133 ctgtcataataaccagctcttagcttggaaggtcgtcatgcaaggaaagtcattaaagttaa 192
 |||||||
 QY 121 gagatcaacgtgtgtcccaatcgtgtgctggaatgcaacgcttcccccgtacatcttggt 180
 |||||||
 DB 193 gagatcaacgtgtgtcccaatcgtgtgctggaatgcaacgcttcccccgtacatcttggt 252
 |||||||
 QY 181 gtccagggtggaagccagctgtcctgcatgtgtgggtgggagagcagacttaacacta 240
 |||||||

DB 253 gtccagggtggaagccagctgtcctgcatgtgtgggtgggagagccgacttaacacta 312
 QY 241 gagccagtgaaacatcatggaactctatctgtgtccaaagaaatccaaagacttacctc 300
 |||||||
 DB 313 gagccagtgaaacatcatggaactctatctgtgtccaaagaaatccaaagacttacctc 372
 |||||||
 QY 301 taccgagcggaacatggtggtcaccctccagacttcgagtcgctgcttaaccgggtgttc 360
 |||||||
 DB 373 taccgagcggaacatggtggtcaccctccagacttcgagtcgctgcttaaccgggtgttc 432
 |||||||
 QY 361 ctgtgacacgtgtgctgaaagccgcatcagctgtcagactcaaccagcttccggaatggt 420
 |||||||
 DB 433 ctgtgacacgtgtgctgaaagccgcatcagctgtcagactcaaccagcttccggaatggt 492
 |||||||
 QY 421 ggcctggaatgcccccatcacagacttctacttcagacagtgtagtag 468
 |||||||
 DB 493 ggcctggaatgcccccatcacagacttctacttcagacagtgtagtag 540
 |||||||

RESULT 5
 Z50812
 ID Z50812 standard; cDNA; 1323 BP.
 AC Z50812;
 XX 31-MAY-2000 (first entry)
 DT Human TANGO-93 CDNA.
 XX TANGO-93; cytokine; human; secreted protein; IL-1 expression; cancer;
 KW Interleukin-1 receptor antagonist; IL-1ra; inflammation; antiasthmatic;
 KW immunosuppressive; antirheumatic; antiarthritic; antipsoriatic; forensic;
 KW antineoplastic; antibacterial; antitumor; cytostatic; immunomodulator;
 KW osteopathic; dermatological; antidiabetic; psoriasis; ulcerative colitis;
 KW graft vs.-host disease; rheumatoid arthritis; inflammatory bowel disease;
 KW septic shock; cachexia; Crohn's disease; chronic myelogenous leukemia;
 KW liver disease; diabetes; osteoarthritis; Hodgkin's disease; Lyme disease;
 KW autoimmune disease; myasthenia gravis; pharmacogenomic; chromosome 2;
 KW diagnosis; asthma; systemic lupus erythematosus; transgenic animal; ss.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 57..524
 FT CDS /tag= a
 FT /product= "Human TANGO-93 protein"
 FT /note= "Has 53% homology to human Interleukin-1 receptor
 FT antagonist (IL-1ra)"
 FT 3'UTR 525..1323
 FT /*tag= b
 XX W0200008045-A2.
 XX 17-FEB-2000.
 PD 06-AUG-1999; 99WO-US17886.
 PF 07-AUG-1998; 98US-0131263.
 PR (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 PA Pan Y;
 PI WPI: 2000-205669/18.
 DR P-PSDB; Y45062.
 XX Isolated nucleic acid sequences encoding TANGO-93 polypeptide useful
 PT for treating a variety of cellular processes e.g. asthma, rheumatoid
 PT arthritis, psoriasis and autoimmune diseases
 XX Claim 2a; Fig 2; 113pp; English.
 PS The present sequence is the cDNA encoding the human TANGO-93, a
 CC

CC secreted protein that belongs to the cytokine superfamily. It plays a
 CC role similar to the secreted interleukin-1 receptor antagonist (IL-1ra)
 CC and its expression is developmentally regulated in the uterus, placenta
 CC and skeletal muscles. Human TANGO-93 gene is mapped to chromosome 2.
 CC Within the IL-1 cluster, TANGO-93 modulates immune mediated inflammation
 CC and IL-1 gene or protein expression. TANGO-93 is useful as a modulating
 CC agent for regulating cellular processes like asthma, graft vs-host
 CC disease, rheumatoid arthritis, psoriasis, inflammatory bowel disease,
 CC septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous
 CC leukaemia, cancer, liver disease, Hodgkin's disease, osteoarthritis,
 CC Lyme disease, cachexia, and autoimmune diseases e.g. myasthenia gravis,
 CC autoimmune diabetes and systemic lupus erythematosus. Partial TANGO-93
 CC sequences are useful in forensic biology, for diagnostic and prognostic
 CC assays, prophylactic and therapeutic treatment and pharmacogenomics. The
 CC DNA sequence is useful as hybridisation probe and primers, for isolation
 CC of TANGO-93 sequence and for the creation of transgenic animals.
 CC
 XX
 XX
 SQ Sequence 1323 BP; 315 A; 338 C; 353 G; 317 T; 0 other;

Query Match 100.0%; Score 468; DB 21; Length 1323;
 Best Local Similarity 100.0%; Pred. No. 5,1e-127;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgtctcgtagtgggagctgtgtctcgaatgaagagctcgagctgaagtgtcttat 60
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB atgtctcgtagtgggagctgtgtctcgaatgaagagctcgagctgaagtgtcttat 116
 QY 61 ctgcataataaccagcttctagctggaagctgcagtcagggaagtcattaaagttaa 120
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB ctgcataataaccagcttctagctggaagctgcagtcagggaagtcattaaagttaa 176
 QY 121 gagatcagctgtgtcccaatcgctgcagtcagtcagccttcccgctatccctgggt 180
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB gagatcagctgtgtcccaatcgctgcagtcagtcagccttcccgctatccctgggt 236
 QY 177 gagatcagctgtgtcccaatcgctgcagtcagtcagccttcccgctatccctgggt 240
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB gtcacaggtgtgaagcagctgtctcatgtgggtgtgggcaagagcgcagcttaacacta 240
 DB gtcacaggtgtgaagcagctgtctcatgtgggtgtgggcaagagcgcagcttaacacta 296
 QY 237 gtcacaggtgtgaagcagctgtctcatgtgggtgtgggcaagagcgcagcttaacacta 296
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB gtcacaggtgtgaagcagctgtctcatgtgggtgtgggcaagagcgcagcttaacacta 300
 QY 241 gtcacaggtgtgaagcagctgtctcatgtgggtgtgggcaagagcgcagcttaacacta 300
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB gtcacaggtgtgaagcagctgtctcatgtgggtgtgggcaagagcgcagcttaacacta 356
 QY 297 gtcacaggtgtgaagcagctgtctcatgtgggtgtgggcaagagcgcagcttaacacta 356
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB gtcacaggtgtgaagcagctgtctcatgtgggtgtgggcaagagcgcagcttaacacta 360
 QY 301 taccgagcgagacatgggggtacacccctcagctcgaatcgagcgcagcgagctgttc 360
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB taccgagcgagacatgggggtacacccctcagctcgaatcgagcgcagcgagctgttc 416
 QY 357 taccgagcgagacatgggggtacacccctcagctcgaatcgagcgcagcgagctgttc 416
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB ctgtgcacagctgtcgaagcagctgtcgaatcgagcgcagcgagctgttc 420
 QY 361 ctgtgcacagctgtcgaagcagctgtcgaatcgagcgcagcgagctgttc 420
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB ctgtgcacagctgtcgaagcagctgtcgaatcgagcgcagcgagctgttc 476
 QY 417 ctgtgcacagctgtcgaagcagctgtcgaatcgagcgcagcgagctgttc 476
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB ggcctggaatggcccccacacacacttctaccagcaatgtgacag 468
 QY 421 ggcctggaatggcccccacacacacttctaccagcaatgtgacag 468
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB ggcctggaatggcccccacacacacttctaccagcaatgtgacag 524

RESULT 6
 250813
 ID 250813 standard; cDNA; 2490 BP.

XX 250813;
 XX 31-MAY-2000 (first entry)

DE Human TANGO-93 cDNA with additional 3'UTR sequence.

KM TANGO-93; cytokine; human; secreted protein; IL-1 expression; cancer;
 KM Interleukin-1 receptor antagonist; IL-1ra; inflammation; antiasthmatic;
 KM immunosuppressive; antirheumatic; antiarthritic; antipsoriasis; asthma;
 KM antineoplastic; antibacterial; antitumor; cyclostatic; immunomodulator;
 KM osteopathic; dermatological; antidiabetic; psoriasis; ulcerative colitis;
 KM graft vs-host disease; rheumatoid arthritis; inflammatory bowel disease;

KM septic shock; cachexia; Crohn's disease; chronic myelogenous leukaemia;
 KM liver disease; diabetes; osteoarthritis; Hodgkin's disease; Lyme disease;
 KM autoimmune disease; myasthenia gravis; pharmacogenomic; diagnosis;
 KM systemic lupus erythematosus; forensic; transgenic animal; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT CDS
 FT
 FT Location/Qualifiers
 FT 63..530
 FT /tag= a
 FT /product= "Human TANGO-93 protein"
 FT /note= "Has 538 homology to human Interleukin-1 receptor
 FT antagonist (IL-1ra)"
 FT 531..2490
 FT /tag= b
 FT /note= "Additional sequences"

XX WO200008045-A2.

XX 17-FEB-2000.

XX 06-AUG-1999; 99MO-US17886.

XX 07-AUG-1998; 98US-0131263.

XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX Pan Y;

XX WPI: 2000-205669/18.

PT Isolated nucleic acid sequences encoding TANGO-93 polypeptide useful
 PT for treating a variety of cellular processes e.g. asthma, rheumatoid
 PT arthritis, psoriasis and autoimmune diseases

PS Example 2; Fig 5; 113pp; English.

CC The present sequence is the cDNA encoding the human TANGO-93, with
 CC additional 3'UTR sequence. It is a secreted protein that belongs to the
 CC cytokine superfamily. It plays a role similar to secreted Interleukin-1
 CC receptor antagonist (IL-1ra). TANGO-93 modulates immune mediated
 CC inflammation and IL-1 gene or protein expression. TANGO-93 is useful as
 CC a modulating agent for regulating cellular processes like asthma, graft
 CC vs-host disease, rheumatoid arthritis, psoriasis, inflammatory bowel
 CC disease, septic shock, ulcerative colitis, Crohn's disease, chronic
 CC myelogenous leukemia, cancer, liver disease, Hodgkin's disease,
 CC osteoarthritis, Lyme disease, cachexia, and autoimmune diseases e.g.
 CC myasthenia gravis, autoimmune diabetes and systemic lupus erythematosus.
 CC Partial TANGO-93 sequences are useful in forensic biology, for diagnostic
 CC and prognostic assays, prophylactic and therapeutic treatment and
 CC pharmacogenomics. The DNA sequences are useful as hybridisation probes
 CC and primers, for isolation of TANGO-93 sequence and for the creation of
 CC transgenic animals.

SQ Sequence 2490 BP; 650 A; 571 C; 619 G; 650 T; 0 other;

Query Match 100.0%; Score 468; DB 21; Length 2490;
 Best Local Similarity 100.0%; Pred. No. 6,4e-127;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgtctcgtagtgggagctgtgtctcgaatgaagagctcgagctgaagtgtcttat 60
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB atgtctcgtagtgggagctgtgtctcgaatgaagagctcgagctgaagtgtcttat 122
 QY 61 ctgcataataaccagcttctagctggaagctgcagtcagggaagtcattaaagttaa 120
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB ctgcataataaccagcttctagctggaagctgcagtcagggaagtcattaaagttaa 182
 QY 121 gagatcagctgtgtcccaatcgctgcagtcagtcagccttcccgctatccctgggt 180
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB gagatcagctgtgtcccaatcgctgcagtcagtcagccttcccgctatccctgggt 242

Sequence 468 BP; 108 A; 128 C; 127 G; 105 T; 0 other;

Query Match	75.0%	Score 351.2	DB 22	Length 466
Best Local Similarity	84.4%	Pred. NO. 4.1e-93		
Matches 395	Conservative 0	Mismatches 73	Indels 0	Gaps 0
QY	1 atggctcctgagctgggagcgctgtgcttcgcgaatgaaagagctgcgcatctgaagtgcttat	60		
	1 atggttcctgagctgggagcactatgtcttcggaagaagagattcagctctgaagtgactggt	60		
Db				
QY	61 ctgcataataaccagctctcagcttgagagggctgcatagcagggaaaggtcattaaagttga	120		
Db	61 ctgcacacataaacacagctctgtctgttgagagagctgcacgcagagaaggtcattaaagttag	120		
QY	121 gagctcaagcgtgggtccccaatcgggtgggtgtgatgacgcacgtctcccccgtatcctgggt	180		
Db	121 gagatcaatgtgtgtccccaatccgggacactggatgacgaatctgtctccctgtctccctgggct	180		
QY	181 gtcccaagggttggaagacccaatgctctgtcattgtgggtgtggggcagaagagccgacattcaacta	240		
Db	181 gtccaaggaggaagccagctgcctactctctgttgggaaagagaagggccaattcttgaacct	240		
QY	241 gaggccatgtaacatcatgagagctctatctctgtgtgcacaaaggaatccaagaagcttcaccttc	300		

Db	241	gagccagtgaaacatcatcagagctctactctcgggccaagaatcaagagcttcaacttc	300
QY	301	taccgcgcggagacatcgaggctcaactccagcttcgagtcgcgcctaacccggctgttc	360
Db	301	taccgcgcggagatcgtgtcttactctccagcttcgaatccgcctcgtaccaccagctgttc	360
QY	361	ctcgagcacggtgctctgagccgatcatgacctgtcaagatccaccagctctcccggaatggt	420
Db	361	ctctgcacatccaccgggaagctgacagacctgttcagtgctcatcctcagatcctctgagacc	420
QY	421	ggtctggaatgtcccatccacagacttctactctccacagctgtgactag	468
Db	421	gctctggagatgtctcccatccacagacttctactctccacagctgtgactag	468

RESULT	9
ID	A09198
	A09198 standard; cDNA: 1275 BP.
XX	
XX	A09198;
XX	
DT	10-AUG-2000 (first entry)
DE	
XX	Murine IL-1 homologue, zllia3 coding sequence.
XX	
KW	Generic; interleukin-1; IL-1; homologue; zllia3; anti-inflammatory;
KW	antagonist; pro-inflammatory; agonist; immunomodulator; antiarthritic;
KW	antiathermatic; osteoprotect; antipsoriatic; antibacterial; cystostatic;
KW	immunosuppressive; antiulcer; antidiabetic; nephrotropic; vasotropic;
KW	vulnerary; Zq14; ss.
XX	
OS	Mus musculus.
XX	
FH	Key
FT	Location/Qualifiers
FT	CDS 101..571
FT	/*tag= a
XX	
PN	MO200020595-A1.
XX	
PD	13-APR-2000.
XX	
PF	08-OCT-1999; 99WO-US23533.
XX	
PR	08-OCT-1998; 98US-0169745.
XX	
PA	(ZYMO) ZYMOGENETICS INC.
XX	
PI	Sheppard PO, West RR, Clegg CH;
PI	
DR	WPI; 2000-303780/26.
DR	P-PSDB; Y92260.
PT	
PT	Proteins useful for treatment of inflammatory conditions as
PT	rheumatoid arthritis and psoriasis are agonists or antagonists forms of
PT	new interleukin-1 homologue
PS	
PS	Example 7; Page 59-60; 64pp; English.
XX	
XX	This DNA encodes an interleukin-1 (IL-1) homologue, designated zllia3.
CC	A 350 bp probe generated from this sequence by PCR using A09199-200 was
CC	used to analyze human northern blots.
CC	It is believed that zllia3 acts through IL-1 receptors. In general,
CC	zllia3 proteins having a Lys residue at position 148 will have
CC	anti-inflammatory activity (e.g. Y92256), whilst those having Asp
CC	(see Y92254) or Glu at this position will have pro-inflammatory action.
CC	zllia3 is used to modulate an immune response in an animal (claimed).
CC	Antagonists zllia3 forms may be used to treat or prevent chronic
CC	inflammatory diseases such as rheumatoid arthritis, osteoarthritis and
CC	Lyme arthritis, psoriasis, to reduce tissue damage after ischemia, to
CC	treat septic shock, graft-versus-host disease and leukemia.
CC	The antagonists may also alleviate inflammatory bowel disease including
CC	Crohn's disease and ulcerative colitis, insulin-dependent diabetes
CC	melittus, acute pancreatitis, glomerulonephritis and cerebral ischemia.

CC Agonist forms of zilla3 may promote wound healing by IL-1 effects on
CC growth factor secretion and cell proliferation. They may also treat
CC infections, especially gastrointestinal infections.

SQ Sequence 1275 BP; 325 A; 315 C; 305 G; 330 T; 0 other;

Query Match	75.0%;	Score 351.2;	DB 21;	Length 1275;
Best Local Similarity	84.4%;	Pred. No. 5.9e-93;		
Matches 395;	Conservative	0;	Mismatches 73;	Indels 0;
				Gaps 0;

[illegible]

RESULT	10
250811	
ID	250811 standard; cDNA; 1360 BP.

AC 250811;

DT 31-MAY-2000 (first entry)

DE Murline TANGO-93 CDNA.

KM TANGO-9 cytokine; mouse; secreted protein; IL1 expression; cancer;
KM Interleukin 1 receptor antagonist; IL-1ra; inflammation; antiasthmatic;
KM Immunosuppressive; antirheumatic; antiarthritis; antipsoriatic; asthma;
KM antinflammatory; antibacterial; anticancer; cytostatic; immunomodulator;
KM osteopathic; dermatologic; antidiabetic; psoriasis; ulcerative colitis;
KM graft vs host disease; rheumatoid arthritis; inflammatory bowel disease;
KM septic shock; cachexia; Crohn's disease; chronic myelogenous leukemia;
KM liver disease; diabetes; osteoarthritis; Hodgkin's disease; Lyme disease;
KM autoimmune disease; myasthenia gravis; pharmacogenomic; diagnosis;
KM systemic lupus erythematosus; forensics; transgenic animal; ss.

05 Mus sp.

.....	Key	Location/Qualifiers
FH	Key	Location/Qualifiers

FT CDS

LE

ET ET

ET

1.3

XX
PN W0200008045-A2

PD 17-FEB-2000

PF 06-AUG-1999; 99WO-US17886.

PR 07-AUG-1998; 98US-0131263.

PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

PI Pan Y;

DR WPI; 2000-205669/18.

XX
XX

PT for treating a variety of cellular processes e.g. asthma, rheumatoid
PT arthritis, psoriasis and autoimmune diseases -

PS Claim 2a; Fig 1; 113pp; English.

CC The present sequence is the cDNA encoding the murine TANGO-93, a secreted
CC protein that belongs to the cytokine superfamily. It plays a role
CC similar to secreted interleukin-1 receptor antagonist (IL-1ra) and its
CC expression is developmentally regulated in liver, heart and bone marrow.
CC TANGO-93 modulates immune mediated inflammation and IL-1 gene or protein
CC expression. TANGO-93 is useful as a modulating agent for regulating
CC cellular processes like asthma, graft vs.-host disease, rheumatoid
CC arthritis, psoriasis, inflammatory bowel disease, septic shock,
CC ulcerative colitis, Crohn's disease, chronic myelogenous leukemia,
CC cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme disease,
CC cancer, and autoimmune diseases e.g. myasthenia gravis, autoimmune
CC diabetes and systemic lupus erythematosus. Partial TANGO-93 sequences
CC are useful in forensic biology, for diagnostic and prognostic assays,
CC prophylactic and therapeutic treatment and pharmacogenomics. The DNA
CC sequences are useful as hybridisation probes and primers, for isolation
CC of TANGO-93 sequence and for the creation of transgenic animals.
XX

SQ Sequence 1360 BP; 374 A; 328 C; 322 G; 336 T; 0 other;

Query Match	75.0%	Score 351.2;	DB 21;	Length 1360;
Best Local Similarity	84.4%	Pred. NO. 6e-93;		
Matches 395; Conservative	0;	Mismatches 73;	Indels 0;	Gaps 0

Oy	1	atggtccctgagctgggagcgtgtgtcttcctccgaatggaagactcgcatttgaagtgcttatt	60
Db	140	atgtctctgagctgggacactatgtcttcctccgaatggaagattcaagcctctgaaagtacttatt	199
Oy	61	ctgcaataataccagcgtctttagctctggaggggtctgtgatactcagggaaggtcattaaagtggaa	120
Db	200	ctgcacaataaacccagctctgtctgtgcgtggaagactctgcacagacagaagatccattaaagtgagag	259
Oy	121	gagatcaacgtgtgtccccaatctgtctggctgtgatactgcagccctgtctccctgcattacttgggt	180
Db	260	gagatcacagtgtgttccccaatctcgggcaactgtgatactgcagctctgtccctgtcatctctgggc	319
Oy	181	gtccaaaggctggaagccagctgcctgtctcatgtgtgggtctgggacagagccagactctaacacta	240
Db	320	gttccaaaggagaagccagctgcctactctgtgtgtggacagagaagaaggtccaaatctgtgaaact	379
Oy	241	gagccagatggaacatcatatgagcttatctgtgtgtccaaaggaatccaaagagcttcaacttc	300
Db	380	gagccaaatggaacatcatatgagcttactctcgtgggtccaaaggaatcaaaagacttcaacttc	439
Oy	301	taccggtcgagacatggggtctcaactccagctctcgaatctcgggtctgtccctaccggggctgtttc	360
Db	440	taccggtcgagataggggtcttactctcaactccagctctcgaatccgtctgtctaccgaagctgtttc	499
Oy	361	ctgtgacaggtgtgcttgaagcccgatctcagctgtctcagactcaaccagcttcccgagaatggt	420
Db	500	ctctctaccactcaaccaggaagctggaacagactcttcaaggtctcaatccagatccctgtgaagaccc	559

XX Mammalian interleukin 1-delta and 1-epsilon - useful for, e.g.
 PT regulating the immune system and inflammatory responses
 XX
 PS Claim 14; Pages 89-90; 113pp: English.

CC This DNA encodes a rodent interleukin (IL)-1 delta polypeptide. The
 CC invention relates to a recombinant polypeptide that specifically binds
 CC polyclonal antibodies (Abs) generated against a 12 consecutive amino acid
 CC segment of IL-1 delta or IL-1 epsilon. Agonists or antagonists of these
 CC IL polypeptides are used to regulate a cell involved in an inflammatory
 CC response. The IL-1 delta or IL-1 epsilon polypeptides and peptides are
 CC used to produce Abs and antigen-Abs complexes. The polypeptides, Abs and
 CC the corresponding nucleic acids regulate development and/or the immune
 CC system, and can be used to diagnose and treat conditions associated with
 CC abnormal expression of IL. Agonists or antagonists of IL-1 delta or IL-1
 CC epsilon polypeptides are used with agonists or antagonists of IL-1 alpha,
 CC IL-1 beta, IL-1 gamma, IL-2 and/or IL-12. The IL-1 delta or IL-1
 CC epsilon polypeptides may be used as a soluble polypeptide or as a fusion
 CC protein with another cytokine or chemokine.

XX Sequence 470 BP; 109 A; 128 C; 127 G; 106 T; 0 other;

Query Match 74.8%; Score 350.2; DB 19; Length 470;
 Best Local Similarity 84.4%; Pred. No. 8e-93;
 Matches 394; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

OY 1 atgtctcgaatggggcgctgtgttcggaatgaagagctggcattgaagtgcttat 60
 DB 4 atgtctcgaatggggcgctgtgttcggaatgaagagctggcattgaagtgcttat 63
 OY 61 ctgcaataaccagctctagctgagcgtgcatgcaggaggaaggaatcaaaagttaa 120
 DB 64 ctgcaataaccagctctgctgctggaagactgcagcagaagaagtgatcaaaagttaa 123
 OY 121 gagatcagctgtgtcccaatcgtgtgctgagtgcacagctgtcccgatccttggt 180
 DB 124 gagatcagctgtgtcccaatcgtgtgctgagtgcacagctgtcccgatccttggt 183
 OY 181 gtccaggtgtgaagcgaatgctgtcattgtgtgtgtgtgtgtgtgtgtgtgtgtgt 240
 DB 184 gtcaagaaggaagcagctgtcattgtgtgtgtgtgtgtgtgtgtgtgtgtgt 243
 OY 241 gagcagaacatcatgagctatctgtgtgccaagagatccaagagcttaacct 300
 DB 244 gagcagaacatcatgagctatctgtgtgccaagagatccaagagcttaacct 303
 OY 301 taccgagcagacatgtggtcactcagctcagctcagctcagctcagctcagct 360
 DB 304 taccgagcagacatgtggtcactcagctcagctcagctcagctcagctcagct 363
 OY 361 ctgtgcaagctgtcgaagccgagatcagctgtcagactcaccagctcccgagaatgt 420
 DB 364 ctgtgcaagctgtcgaagccgagatcagctgtcagactcaccagctcccgagaatgt 423
 OY 421 ggcctgaatgcccccatcacagactctactctcagcagctgtgacta 467
 DB 424 ggcctgaatgcccccatcacagactctactctcagcagctgtgacta 470

RESULT 13
 X89431
 ID X89431 standard; DNA; 468 BP.

XX X89431;
 AC
 XX
 DT 28-SEP-1999 (first entry)
 XX
 DE Mouse interleukin 1 delta encoding DNA.
 XX
 KW Interleukin 1 delta; IL-1 delta; glaucoma; ectodermal dysplasia;
 insulin-dependent diabetes mellitus; wrinkly skin syndrome;

KW T-cell leukemia; lymphoma; tibial muscular dystrophy; ss.
 XX
 OS Mus musculus.

EH Key Location/Qualifiers
 FT CDS 1..468
 FT /*tag= a
 FT /product= "IL-1 delta"
 FT /note= "no stop codon given"

PN W09935268-A1.
 XX
 XX 15-JUL-1999.
 XX
 XX 08-JAN-1999; 99WO-US00514.
 PF
 XX
 PR 01-JUN-1998; 98US-0087393.
 PR 09-JAN-1998; 98US-0071074.
 XX
 XX (IMMV) IMMUNEX CORP.

XX Sins JE;
 XX WPI: 1999-458310/38.
 DR P-PSDB: Y28407.
 XX

PT Murine and Human Interleukin 1 delta DNA, polypeptides and its
 fragments, useful as molecular weight markers
 XX
 XX Claim 1; Page 66; 72pp: English.

CC The present sequence encodes mouse interleukin 1 delta (IL-1 delta).
 CC IL-1 delta proteins are useful for the determination of the molecular
 CC weight of a sample protein. The protein and its fragments are useful as
 CC controls for peptide fragmentation. This is useful for determining the
 CC isoelectric point of a sample protein. Antibodies generated against
 CC IL-1 delta and its fragmented peptides can be used to enhance the
 CC accuracy of these molecular weight markers to determine the apparent
 CC molecular weight and isoelectric point of a sample protein. IL-1 delta
 CC can be used to screen for potential inhibitors of activity associated
 CC with IL-1 delta counter-structure molecules. IL-1 delta can also be used
 CC as therapeutic agents for the treatment of diseases mediated by IL-1
 CC delta. IL-1 delta may be used as a reagent in studying the interleukin 1
 CC (IL-1) signalling pathway, or as a reagent to block IL-1 signalling. The
 CC IL-1 delta coding sequences can be used to identify human chromosome 2,
 CC and to identify genes associated with certain diseases, especially with
 CC region 2q11-12, including glaucoma, ectodermal dysplasia, insulin-
 CC dependent diabetes mellitus, wrinkly skin syndrome, T-cell leukemia/
 CC lymphoma and tibial muscular dystrophy.

SO Sequence 468 BP; 108 A; 128 C; 127 G; 105 T; 0 other;

Query Match 74.4%; Score 348.2; DB 20; Length 468;
 Best Local Similarity 84.3%; Pred. No. 3e-92;
 Matches 392; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

OY 1 atgtctcgaatggggcgctgtgttcggaatgaagagctggcattgaagtgcttat 60
 DB 4 atgtctcgaatggggcgctgtgttcggaatgaagagctggcattgaagtgcttat 63
 OY 61 ctgcaataaccagctctagctgagcgtgcatgcaggaggaaggaatcaaaagttaa 120
 DB 64 ctgcaataaccagctctgctgctggaagactgcagcagaagaagtgatcaaaagttaa 123
 OY 121 gagatcagctgtgtcccaatcgtgtgctgagtgcacagctgtcccgatccttggt 180
 DB 124 gagatcagctgtgtcccaatcgtgtgctgagtgcacagctgtcccgatccttggt 183
 OY 181 gtccaggtgtgaagcgaatgctgtcattgtgtgtgtgtgtgtgtgtgtgtgtgtgt 240
 DB 184 gtcaagaaggaagcagctgtcattgtgtgtgtgtgtgtgtgtgtgtgtgtgt 243

QY 241 gaggcagtgaaacatcatgagctctatctgtgtgccaaagaaatccaagcttcaccttc 300
 |||||
 Db 244 gaggcagtgaaacatcatgagctctacctctcgggccaagaaatccaagcttcaccttc 303
 QY 301 taccgcggggaacatgggtccacctcagcttgatgcgttcctaccgggctgttc 360
 |||||
 Db 304 taccgcggggaataggctctaccctcagcttcgaatccgtctaccacagctgttc 363
 QY 361 ctgtgacaggtgctcgaacccatcagctctcagactcaccagcttcgggaatgt 420
 |||||
 Db 364 ctctgacactcaacggaaagctgacacagcctgtcaggtcctacatccctcgaagaccc 423
 QY 421 ggcctggaatgcccccacacagactctccttcacacagatgtgac 465
 |||||
 Db 424 ggcctggaatgcccccacacagactctccttcacacagatgtgac 468
 RESULT 14
 ID A09194 standard; DNA; 465 BP.
 AC A09194;
 XX
 XX 10-AUG-2000 (first entry)
 DE Human IL-1 homologue, hz11a3 degenerate coding sequence.
 XX
 KW Generic: Interleukin-1; IL-1; homologue; z11a3; anti-inflammatory;
 KW antagonist; pro-inflammatory; agonist; immunomodulator; antiarthritic;
 KW antirheumatic; osteopathic; antipsoriatic; antibacterial; cycostatic;
 KW immunosuppressive; antitumor; antidiabetic; nephrotropic; vasotropic;
 KW vulnerability; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200020595-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 08-OCT-1999; 99WO-US23533.
 XX
 PR 08-OCT-1998; 98US-0169745.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sheppard PO, West RR, Clegg CH;
 XX
 DR MPI: 2000-303780/26.
 DR P-PSDB; Y92257.
 XX
 XX Proteins useful for treatment of inflammatory conditions such as
 PR rheumatoid arthritis and psoriasis are agonists or antagonists forms of
 PT new interleukin-1 homologue
 XX
 PS Disclosure: Page 57; 64pp; English.
 XX
 XX This DNA encodes an interleukin-1 (IL-1) homologue, designated z11a3.
 CC It is believed that z11a3 acts through IL-1 receptors. In general,
 CC z11a3 proteins having a lys residue at position 148 will have
 CC anti-inflammatory activity (e.g. Y92256), whilst those having Asp
 CC (see Y92254) or Glu at this position will have pro-inflammatory action.
 CC z11a3 is used to modulate an immune response in an animal (claimed).
 CC Antagonists z11a3 forms may be used to treat or prevent chronic
 CC inflammatory diseases such as rheumatoid arthritis, osteoarthritis and
 CC Lyme arthritis, psoriasis, to reduce tissue damage after ischemia, to
 CC treat septic shock, graft-versus-host disease and leukemia.
 CC The antagonists may also alleviate inflammatory bowel disease including
 CC Crohn's disease and ulcerative colitis, insulin-dependent diabetes
 CC mellitus, acute pancreatitis, glomerulonephritis and cerebral ischemia.
 CC Agonist forms of z11a3 may promote wound healing by IL-1 effects on
 CC growth factor secretion and cell proliferation. They may also treat
 CC infections, especially gastrointestinal infections.
 CC
 XX

SQ Sequence 465 BP; 70 A; 45 C; 86 G; 67 T; 197 other;
 Query Match 70.7%; Score 330.8; DB 21; Length 465;
 Best Local Similarity 57.6%; Pred. No. 3.6e-87;
 Matches 268; Conservative 108; Mismatches 89; Indels 0; Gaps 0;
 QY 1 atgtcctcgtatggcgcgtgtgtctccgaatgaagactcgcattgaagtgttat 60
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 Db 1 atgtcttynmsngngnctnbtgtytymnatgaatgawtngcnynatargtynntay 60
 QY 61 ctgcataataacacagctctcagcttgaggctgacgtacgaggaagtcattaaagtga 120
 |||||
 Db 61 ytncaayaayaarytynlngcngngngnytncaaycngngaargtnahtaargngar 120
 QY 121 gagataagcgtgtgtcccaatcgtgtcgtgagatgcacgctgtcccccgtatccctgg 180
 |||||
 Db 121 garatnmsngltngtncncaaymngntggtngaygcmsnynmsncngtnathtnngn 180
 QY 181 gtccaggttgaaagccagctgtcaltggtggtggtgagcagagcagctcactaacta 240
 |||||
 Db 181 gtncargngngmwnsncarctgytnwsntgtygngtngncargcncnynacnyn 240
 QY 241 gaggcagtgaaacatcatgagctctatctgtgtgccaaagaaatccaagcttcaccttc 300
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 Db 241 garcngtnaayathatgagrytnlaytngngngcnaargawnaarwntlyacntly 300
 QY 301 taccgcggggaacatgggtccacctcagcttcagatcgtcgtcgcgcgggctgtgttc 360
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 Db 301 taymgmgngayayaltggytnacnwsnhtlygarwngngcngctaycngngntgltly 360
 QY 361 ctgtgacaggtgctcgaacccagctcagctgtcagactcaccagcttcggagaatgt 420
 |||||
 Db 361 ytnlyacngtngcngcargngcngcngcngtngmgytnaencarytnncngnaayaagn 420
 QY 421 ggcctggaatgcccccacacagactctccttcacacagatgtgac 465
 |||||
 Db 421 gnttggaaaygcncnathacngaytlytlycarcartygag 465
 RESULT 15
 ID A09195 standard; DNA; 465 BP.
 AC A09195;
 XX
 XX 10-AUG-2000 (first entry)
 DE Human IL-1 homologue, hz11a3-K148, degenerate coding sequence.
 XX
 KW Generic: Interleukin-1; IL-1; homologue; z11a3; anti-inflammatory;
 KW antagonist; pro-inflammatory; agonist; immunomodulator; antiarthritic;
 KW antirheumatic; osteopathic; antipsoriatic; antibacterial; cycostatic;
 KW immunosuppressive; antitumor; antidiabetic; nephrotropic; vasotropic;
 KW vulnerability; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200020595-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 08-OCT-1999; 99WO-US23533.
 XX
 PR 08-OCT-1998; 98US-0169745.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sheppard PO, West RR, Clegg CH;
 XX
 DR MPI: 2000-303780/26.
 DR P-PSDB; Y92256.
 XX

PT Proteins useful for treatment of inflammatory conditions such as
PT rheumatoid arthritis and psoriasis are agonists or antagonists forms of
PT new interleukin-1 homologue
XX

PS Disclosure: Page 57-58; 64pp; English.

CC This degenerate DNA encodes a variant Interleukin-1 (IL-1) homologue,
CC designated zllia3-K148. It is believed that zllia3 acts through IL-1
CC receptors. In general, zllia3 proteins having a Lys residue at position
CC 148 will have anti-inflammatory activity, whilst those having Asp (see
CC Y92254) or Glu at this position will have pro-inflammatory action.
CC Zllia3 is used to modulate an immune response in an animal (claimed).
CC Antagonists zllia3 forms may be used to treat or prevent chronic
CC inflammatory diseases such as rheumatoid arthritis, osteoarthritis and
CC Lyme arthritis, psoriasis, to reduce tissue damage after ischemia, to
CC treat septic shock, graft-versus-host disease and leukemia.
CC The antagonists may also alleviate inflammatory bowel disease including
CC Crohn's disease and ulcerative colitis, insulin-dependent diabetes
CC mellitus, acute pancreatitis, glomerulonephritis and cerebral ischemia.
CC Agonist forms of zllia3 may promote wound healing by IL-1 effects on
CC growth factor secretion and cell proliferation. They may also treat
CC infections, especially gastrointestinal infections.

XX
SQ Sequence 465 BP; 71 A; 45 C; 85 G; 67 T; 197 other;

Query Match 70.1%; Score 328; DB 21; Length 465;

Best local similarity 57.4%; Pred. No. 2.4e-86;

Matches 267; Conservative 107; Mismatches 91; Indels 0; Gaps 0;

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DB 1 atgctcctgagtgaggcgctgctccgaatgaagagctcgacatgaagtgcttat 60
QY 61 ctgcatataacagactctcagtgagtgagtgagtgagtgagtgagtgagtgag 120
DB 61 ctgcatataacagactctcagtgagtgagtgagtgagtgagtgagtgagtgag 120
QY 121 gagatcagcgtgctgctccgaatgaagagctcgacatgaagtgagtgagtgag 180
DB 121 gagatcagcgtgctgctccgaatgaagagctcgacatgaagtgagtgagtgag 180
QY 181 gtcacaggtgagagcagtgctgctcagtgagtgagtgagtgagtgagtgagtgag 240
DB 181 gtcacaggtgagagcagtgctgctcagtgagtgagtgagtgagtgagtgagtgag 240
QY 241 gaggcagtgagagcagtgctgctcagtgagtgagtgagtgagtgagtgagtgag 300
DB 241 gaggcagtgagagcagtgctgctcagtgagtgagtgagtgagtgagtgagtgag 300
QY 301 tacggcgagagcagtgctgctcagtgagtgagtgagtgagtgagtgagtgagtgag 360
DB 301 tacggcgagagcagtgctgctcagtgagtgagtgagtgagtgagtgagtgagtgag 360
QY 361 ctgtgacagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 420
DB 361 ctgtgacagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 420
QY 421 ggtgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 465
DB 421 ggtgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 465

Search completed: May 31, 2001, 08:19:15
Job time: 2544 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 31, 2001, 06:35:20 ; Search time 1132.2 Seconds
(without alignments)
3611.106 Million cell updates/sec

Title: us-09-612-921-3

Perfect score: 468
Sequence: 1 atggctcgtgagtgaggcgcgt.....acttcagcagtgtagctag 468

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

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3: gb_est3:*
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 234: em_gss_vrt37:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	208.6	44.6	382	W08205	W08205 mb49b11.r1
2	108.6	23.2	938	BE563703	BE563703 601335323
3	97.6	20.9	531	AM951593	AM951593 EST136363
4	95.8	20.5	397	BE846054	BE846054 232365 BA
5	95.6	20.4	635	AM262191	AM262191 xg62f01.x
6	94.6	20.2	435	W78043	W78043 zdt72d01.r1
7	94	20.1	549	BE706905	BE706905 QV0-HT036
8	93.6	20.0	508	AM464284	AM464284 BP230015A
9	90.6	19.4	1020	BE245180	BE245180 602357579
10	89	19.0	281	R50241	R50241 yf58a03.r1
11	87.6	18.7	260	R46871	R46871 yf54f05.r1
12	84	17.9	356	BE477245	BE477245 160853 BA
13	66.8	14.3	976	BE563442	BE563442 601335496
14	62.8	13.4	468	BF350044	BF350044 CM1-HT024
15	61.6	13.2	554	AI391145	AI391145 mc16c06.y
16	61	13.0	602	AM083357	AM083357 xc08g03.x
17	55.2	11.8	551	BE058746	BE058746 na10a11.
18	53	11.3	689	AA768860	AA768860 n275f12.s

19	52.8	11.3	870	145	BF244205	601863146
c	20	51.4	11.0	539	148	BF4333375
c	21	50.2	10.7	354	158	W20594
c	22	49.2	10.5	436	114	AM361164
c	23	49.2	10.5	536	120	AM853610
c	24	49.2	10.5	539	114	AM366430
c	25	49.2	10.5	553	114	AM3661172
c	26	49.2	10.5	555	138	BE595960
c	27	49.2	10.5	557	114	AM366437
c	28	49.2	10.5	559	117	AM578451
c	29	48.6	10.4	547	10	AA704518
c	30	48.4	10.3	533	174	BC231663
c	31	42	9.0	560	114	AM361245
c	32	41.6	8.9	802	149	BF534817
c	33	41.2	8.8	401	135	R34906
c	34	41.2	8.8	442	159	W95637
c	35	40.8	8.7	349	6	AA381142
c	36	40.2	8.5	434	119	AM753217
c	37	40	8.5	410	168	BF731619
c	38	40	8.5	498	114	AM379511
c	39	39	8.3	779	112	AM211461
c	40	38.4	8.2	509	172	BC058520
c	41	38	8.1	862	107	AU140167
c	42	37.8	8.1	539	165	BE299069
c	43	37.6	8.0	288	14	AF054165
c	44	36.8	7.9	191	114	AM367148
c	45	36	7.7	862	136	BE567173
						BF244205 601863146
						BF4333375
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						AM853610 RC1-CT025
						AM366430 CM3-HT019
						AM3661172 RC1-CT025
						BE595960 RC1-CT025
						AM366437 CM3-HT019
						AM578451 RC1-CT025
						AA704518 z13b07.s
						BC231663 na137e09.
						AM361245 RC1-CT025
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						AA381142 EST94184
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						BF731619 mab89b04.
						AM379511 CM2-HT024
						AM211461 na1c09.y
						BC058520 u015f01.
						AU140167 AU140167
						BE299069 601089020
						AF054165 AF054165
						AM367148 MKO-HT015
						BE567173 601341360

ALIGNMENTS

RESULT	1				
W08205					
LOCUS	W08205	382 bp	mRNA	EST	05-SEP-1996
DEFINITION	mb49b11.r1 Soares mouse p3JMF19.5 Mus musculus cDNA clone				

ORGANISM	REFERENCE
<i>Mus musculus</i>	1 (bases 1 to 382)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,	

TITLE	JOURNAL	COMMENT
The WashU-HHMI Mouse EST Project	Unpublished (1996)	Contact: Maria W/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:214133 Seq primer: ETPPrimer High quality sequence stop: 354. Location/Qualifiers I..382

Query Match	44.6%;	Score 208.6;	DB 157;	Length 382;
Best Local Similarity	84.2%;	Pred. No. 2.1e-47;		
Matches 235;	Conservative 0;	Mismatches 44;	Indels 0;	Gaps 0;

OY	1	atgtcctcgtagtgaggcgctgtccttcgcgaatgaagaagctcgcatgaagtgctttat	60
Db	104	ATGGTTCAGACTGAGGGGCGCACTTGCCTTCGCAATGGAAGGATTCAGCGTCACTGTAT	163
OY	61	ctgcataataaccgagctctagctggagaggttgatgcatggaagaggttcattaaaggtgaa	120
Db	164	CTGCACAAATTAACGAGCTCTCGCTGAGAGACTGCACGACGAGGAAGGTCATTAAAGGTGAG	223

BASE COUNT	92 a	86 c	103 g	101 t
------------	------	------	-------	-------

ORIGIN

/note=Vector: pUT3D (Pharmacia) with a modified polylinker. Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - 0.150(GT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCGCAATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pUT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."

Qy 241 gagccagtgacaatcattcgtctatctctgtgtgccaag 279
|||||
Db 344 GAGCCAGTGAACATCATGTGAGCTCTACTCGGGGCGCAAG 382

RESULT	2			
LOCUS	BE563703			
DEFINITION	BE563703	938 bp	mRNA	EST 15-AUG-2000
ACCESSION	601335322F1	NIH_MGC_39	Homo sapiens	CDNA clone IMAGE:3689284 5',
VERSION	BE563703			mRNA sequence.
KEYWORDS	BE563703.1	GI:9807423		
SOURCE	EST.			
ORGANISM	human.			
REFERENCE	Homo sapiens			
AUTHORS	Eukaryotic: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
TITLE	Mammalia: Eutheria; Primates; Catarrhini; Homnidae; Homo.			
JOURNAL	1 (bases 1 to 938)			
COMMENT	NIH-MGC http://mgc.nci.nih.gov/ .			
	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			
	Tel: (301) 496-1550			
	Email: Robert.Strausberg@nih.gov			
	Tissue Procurement: ATCC			
	CDNA Library Preparation: Ling Hong/Rubin Laboratory			
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
	Clone distribution: Incyte Genomics, Inc.			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LLNL at:			
	http://image.llnl.gov			
	Plate: L10M583 row: n column: 05			
	High quality sequence stop: 764.			

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FEATURES
source
Location/Qualifiers
1. .938
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3689284"
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/clone.lib="NIH.MCC.39"
 /lib.type="adenocarcinoma"
 /lab.host="DH10B (phage-resistant)"
 /note="Organ: pancreas; Vector: pOTB7; Site:1: XhoI;
 Site:2: EcoRI; cDNA made by oligo-dT priming.
 directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed
 by Ling Hong in the laboratory of Gerald M. Rubin
 (University of California, Berkeley) using ZAP-cDNA
 synthesis kit (Stratagene) and Superscript II RT (Life
 Technologies)."

BASE COUNT 226 a 283 c 232 g 197 t
 ORIGIN

Query Match 23.2%; Score 108.6; DB 136; Length 938;
 Best Local Similarity 58.6%; Pred. No. 1.3e-19;
 Matches 236; Conservative 0; Mismatches 149; Indels 18; Gaps 2;

24 ctccgaatgaagagctcgcatgaagtgcttatactgtcataataaccagctctacg 83
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 67 cttcagaatctggatgtaaccagaaaccttctatctgaggaacacacactagttgc 126
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 84 tggagggctgcatacgaggaaggtcattaaaggtgaagacagcgtgtgcccaatcg 143
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 127 cggatctctgcaagagcacaatgtctaatattagaaagaaagatagatgtgtaaccattga 186
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 144 gtggtgtgattgcagcctgtcccccgtatcctctgtgtgtccaggtgtggaagcagtgct 203
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 187 gccctatgtctc-----tggtcttggaatccatgagggagaaatgtgctt 231
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 204 gcatatgtgtgtg---gggcagagagccagacttaacacatagagccagtgtaacatcgtga 260
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 232 gtctctgtgtcagtgctgtgatgagacacagactccagctggagggcagtttaacatcgtga 291
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 261 gctctatctgtgtgcgaagaatccaagagcttcaaccttcaaccgagcgaggaatggagct 320
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 292 cctgagcgaagacagaaacagacagacagacgcttccgcttccatccgctcagacagtgccccc 351
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 321 caactccagctcgatgt 380
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 352 caccacacagctgt 411
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 381 cgatcagcctgtcagactcaccacagcttcccgagaatgtgtgc 423
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 412 tgaccagcccgctgacgctcaccatattgcttgcagcagagcgctc 454
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 3
 LOCUS AW951593 531 bp mRNA EST 01-JUN-2000
 DEFINITION EST36363 MAGE resequences, MAGB Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW951593
 VERSION AW951593.1 GI:8141270
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 AUTHORS Hedde, P., Qi, R., Abernathy, K., Dharap, S., Caspard, R., Gay, C., Holt
 I.E., Saeed, A.I., Sharov, Y., Lee, N.H., Yeatman, T.J. and
 Quackenbush, J.

TITLE Assessment of gene expression patterns in a model of colon tumor
 metastasis using a 19,200 element cDNA microarray
 JOURNAL Unpublished (2000)
 COMMENT The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 3528
 Fax: 301 838 0208
 Email: johnnet@tigr.org
 Plate: 29

Seq primer: Reverse.
 Location/Qualifiers
 source
 1..531
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone.lib="MAGE resequences, MAGB"
 /note="Vector: pluscriptskm"

BASE COUNT 143 a 145 c 120 g 123 t
 ORIGIN

Query Match 20.9%; Score 97.6; DB 122; Length 531;
 Best Local Similarity 56.7%; Pred. No. 1.3e-16;
 Matches 230; Conservative 0; Mismatches 159; Indels 17; Gaps 2;

24 ctccgaatgaagagctcgcatgaagtgcttatactgtcataataaccagctctacg 83
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 115 cttcagaatctggatgtaaccagaaaccttctatctgaggaacacacactagttgc 174
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 84 tggagggctgcatacgaggaaggtcattaaaggtgaagacagcgtgtgcccaatcg 143
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 175 tggatctctgcaagagcacaatgtctaatattagaaagaaagatagatgtgtaaccattg- 233
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 144 gtggtgtgattgcagcctgtcccccgtatcctctgtgtgtccaggtgtggaagcagtgct 203
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 234 -----accctatgctcatgtcttggaattcccttgaagaaagatgtgctt 280
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 204 gtcattgt---gggtggggcagagagccagacttaacacatagagccagtgtaacatcgtga 260
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 281 gtctctgttcaagtgtgtgatgagacacagactccagctggagggcagtttaacatcgtga 340
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 261 gctctatctgtgtgcgaagaatccaagagcttcaaccttcaaccgagcgaggaatggagct 320
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 341 cctgagcgaagacaaacagacagacagcgttcccttccatccgctcagacagcggtcc 400
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 321 caactccagctcgatgt 380
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 401 caccacacagctgt 460
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 381 cgatcagcctgtcagactcaccacagcttcccgagaatgtgtgtgc 426
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 461 tgaccagcccgctgacgctcaccatattgcttgcagcagacgttaattg 506
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
 LOCUS BE846054 397 bp mRNA EST 25-SEP-2000
 DEFINITION 232365 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION BE846054
 VERSION BE846054.1 GI:10282878
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.

REFERENCE
 AUTHORS Sonstegard, T.S., Capuco, A.V., Van Tassel, C.P., Ashwell, M.S. and
 Wells, K.D.

TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary
 gland cDNA library
 JOURNAL Unpublished (2000)
 COMMENT Contact: Sonstegard TS
 USDA, ARS, Beltsville Agricultural Research Center
 Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
 Tel: 301 504 8416
 Fax: 301 504 8414
 Email: tadsl@ps1.barc.usda.gov

Single pass sequencing. Bases called and alt-trimmed with phred
 v0.980904.e. Vector identified by cross-match with the -minscore 18
 and -minmatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCACGACGACG
 Plate: 114 row: E column: 10
 Seq primer: ATTAGTGACACTATAG.
 Location/Qualifiers

FEATURES
 source
 1..397

/organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="BARC 5BOV"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPOR6; Site_1: XbaI; Site_2: XhoI;
 Library made from pooled mRNA isolated from mammary
 tissues at eight physiological, developmental, and disease
 states."

BASE COUNT
 ORIGIN
 88 a 105 c 122 g 82 t

Query Match 20.5%; Score 95.8; DB 140; Length 397;
 Best Local Similarity 89.6%; Pred. No. 3.9e-16;
 Matches 103; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1 atggcctcgaagggggcgtgcttcgcaatgaaggaactcgagcttgagtgctttat 60
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 247 ATGGCTCTGAGGGGGCGCTGCTTCGATGAAGGATGCAATGAGGCTTATAC 306

OY 61 ctgcataataacagctctagctgagggcgtcatgacgaggaaggtcattaaag 115
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 307 CTGCATGAATACAGCTTCTACCGGAGCCCTACAAAGCGGGAAGGTCAATTAAG 361

RESULT 5

AM262191 635 bp mRNA EST 28-DEC-1999
 LOCUS x962f01.x1 NCI CGAP HN9 Homo sapiens cDNA clone IMAGE:2755225 3'
 DEFINITION similar to gb:X64532.rnal INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN
 PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION
 VERSION AM262191
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 1 (bases 1 to 635)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL
 COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Edward Shillitoe Ph.D., Silvio Gutkind Ph.D.,
 Chidchanok Leethanakul D.D.S., Michael Emmert-Buck M.D. Ph.D.,
 cDNA Library Preparation: David B. Krizman, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNI at:
 www.bio.lnl.gov/bdrp/image/image.html

FEATURES
 source
 Possible reversed clone: polyT not found
 Seq primer: -40UP from Gibco
 High quality sequence stop: 421.
 Location/Qualifiers
 1..635

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="IMAGE:2755225"
 /clone_lib="NCI CGAP HN9"
 /tissue_type="normal squamous epithelium from retromolar
 trigone"
 /lab_host="DH10B"

/note="Vector: pAMP10; cDNA made by oligo-dT priming.
 Non-directionally cloned into the UDG sites of pAMP10.
 Size-selected on agarose gel, average insert size 500 bp.
 Primary library: non-amplified. cDNA library
 preparation: David B. Krizman, Ph.D (NCI). Reference:
 Krizman et al. (1996) Cancer Research 56:5380-5383."

BASE COUNT
 ORIGIN
 135 a 208 c 159 g 133 t

Query Match 20.4%; Score 95.6; DB 113; Length 635;
 Best Local Similarity 63.8%; Pred. No. 4.9e-16;
 Matches 162; Conservative 0; Mismatches 16; Indels 3; Gaps 1;

OY 173 tcttggtgtccagaggtggaagccagctgctctcatgtg---gggtggggcagagccga 229
 || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 34 TCTTGGGAATCCATGAGGAGGAAGATGTGCTTCTCTGTCTCAAGTCTGTATGACACCA 93

OY 230 ccttaacactagagccagtgaaatcatatgagctctatcttggtgccaagaatccaaga 289
 || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 94 GACTCCAGCTGAGCGAGCACTTAACATCATGACCTGAGCGAGAAACAGAGACCAAGC 153

OY 290 gcttaacctctacccggcgagacatagggctactctcagcttgagtgctgcttacc 349
 ||||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 154 GCTTGCCTTCATCCGCTCAGACAGTGGCCACCAAGTTTATGCTTGCCGCTGCC 213

OY 350 cgggctggtctctgtagcaggtgacctgaagccatcagcttcagactaccacagcttc 409
 || ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 214 CCGGTGTTGTTCTCTCTGACAGGATGGAAGTGCAGGAGCCGCTCAGCCATATATGC 273

OY 410 ccgagaatggtgac 423
 || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 274 CTGACGAGCGCTC 287

RESULT 6

W78043 435 bp mRNA EST 17-OCT-1996
 LOCUS zd72d01.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
 DEFINITION IMAGE:346177 5', similar to gb:X64532.rnal INTERLEUKIN-1 RECEPTOR
 ANTAGONIST PROTEIN PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION
 VERSION W78043
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 1 (bases 1 to 435)
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
 M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
 Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston
 R., Williamson, A., Wohlmann, P. and Wilson, R.
 The WashU-Merck EST Project

JOURNAL
 COMMENT Unpublished (1995)
 Contact: Wilson RK
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through ILNI; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert length: 813 Std Error: 0.00
 Seq primer: mob.REGA+ET

FEATURES
 source
 Location/Qualifiers
 1..435

/organism="Homo sapiens"
 /db_xref="GDB:1271552"
 /db_xref="taxon:9606"
 /clone_image="IMAGE:346177"
 /clone_lib="Soares_fetal_heart_NbHH19W"
 /sex="unknown"

Fax: 217 244 5617
Email: h-lewin@uic.edu

Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmi g: Sequences match from Washington University Genome Center PHRAP suite. Sequences submitted are vector free and at least 200 bp in length.

PCR primers

FORWARD: TAATACGCTCATATAGG

BACKWARD: ATTACCCCTCAATAG

Insert length: 508 Std Error: 0.00

Plate: BP230015420 row: F column: 10

Seq primer: AGCGGATACAAATTCACACAGGA

High quality sequence stop: 508.

Location/Qualifiers

1. 508

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone="BP230015420F10"

/clone_lib="Soares normalized bovine placenta"

/sex="Female"

/lab_host="DHI10B"

/note="Organ: placenta; Vector: pTR73Pac; Site:1: EcorI; Site:2: NotI; The cDNA library was contributed by the Soares Laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806."

BASE COUNT 126 a 148 c 127 g 107 t

ORIGIN

Query Match 20.0%; Score 93.6; DB 115; Length 508;
Best Local Similarity 56.2%; Pred. No. 1.7e-15;
Matches 227; Conservative 0; Mismatches 159; Indels 18; Gaps 2;

11 gtggggcgtgtgtcttcgaatgaagcctggcattgaagtgcttattctgcatata 70
Db 4 GCGAGATCGAAGCCCTTCAGAGATCTGGATGTCACCAAGAGATCTTCACGAGAA 63
QY 71 accagcttcagctgaagcctgacagcaggaagtcattcaagtgtaagagcagc 130
Db 64 ACCAATTAGTGTGCTGATCTTGAAGCAAGCAATTAATTAAGGAGAGATGATG 123
QY 131 tgggtcccaatcggtgtgtgacagcctgtcccgctacccctgggtgtccaggtg 190
Db 124 TGGTACCA-----TCGAACCCCATATATGTTCTGGGGATCCATGGGG 168
QY 191 gaagccagctgtcgtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 247
Db 169 GGAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 228
QY 248 tgaacatcatgagctgtatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 307
Db 229 TGAACATCATGACTTGAACCAAGAACAGGACGACGACGACGCTTTCCTTCATCCGCT 288
QY 308 gggagatggt 367
Db 289 TCGAACAGGGGGCCACCAAGCCTTTGAGTCAAGTGTGCTGCTGCTGCTGCTGCA 348
QY 368 cgt 411
Db 349 CATCACTGTGAGGCGGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 392

RESULT 9
BG245180 1020 bp mRNA EST 13-FEB-2001
LOCUS 602357579F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4486098 5',
DEFINITION mRNA sequence.
ACCESSION BG245180
VERSION BG245180.1 GI:12754995
KEYWORDS EST.

SOURCE

house mouse;

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 1020)

NIH-MGC <http://mgs.nci.nih.gov/>.

Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNLN at:

<http://image.llnl.gov>

Plate: LNLN10328 row: n column: 19

High quality sequence start: 4

High quality sequence stop: 653.

FEATURES

source

1. 1020

/organism="Mus musculus"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:4486098"

/clone_lib="NCI CGAP_Mam1"

/tissue_type="tumor, biopsy sample"

/dev_stage="3 months, virgin"

/lab_host="DHI10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI; Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 282 a 269 c 268 g 201 t

ORIGIN

Query Match 19.4%; Score 90.6; DB 174; Length 1020;
Best Local Similarity 56.2%; Pred. No. 1.3e-14;
Matches 221; Conservative 0; Mismatches 154; Indels 18; Gaps 2;

24 ctccgaatgaagcctgagcctgagctgttattctgtcataaaccagcttctagc 83
Db 157 CTTGAGATCTGAGTACTAATCAAGACGACCTTTTACCTGAGAAACACACAGCTATTGC 216
QY 84 tggaggt 143
Db 217 TGGTACTTACAGGACCAAAATATCAAACTAGAAAGAAAGTTAGCATGTGCTATTGA 276
QY 144 gt 203
Db 277 -----CCTTCATAGTGTGTGTTCTTGGGATCCACGGGGCAAGCTGTGCTT 321
QY 204 gtcatgtg---gggt 260
Db 322 GTCTGTGCGCAAGTGTGAGATGATATCAAGCTCCAGCTGGAGGAAATTACATCATGA 381
QY 261 gctctattctgt 320
Db 382 TCTGAGCAAGAAACAAAGAAAGAAAGCAAGCGCTTTCCTTCATCCGCTGTGAGAAAGGCC 441
QY 321 caccctcagctgt 380
Db 442 CACCAACAGCTTTGAGTACGCTGCTGTCCAGATGATGTTCTCTGCAACACTAGAGGC 501
QY 381 cgtatcagctgtcagactaccagcagcttccga 413
Db 502 TGACCGTCTGTGAGCTTCACCAACACACCGGA 534

RESULT 10

[illegible][illegible]

QY 337 tggcgcttaccgagcgctgctgctgcaaggtgctgaagcagatcagctgtcaga 396
DB 142 TCGCGGCTGCGCCCGGTTGCTCTCTCTGACGAGTGAGGCTGACGACCGCTCAGC 201
QY 397 ctacccagctcccgagagatgtgac 423
DB 202 CTCACCAATATGCTGCTGACGAGCGCTC 228

RESULT 12

LOCUS BE477245 356 bp mRNA EST 28-AUG-2000

DEFINITION BE477245 160853 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION BE477245 GI:9596778

VERSION EST.

KEYWORDS EST.

SOURCE cow.

ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Bovidae; Bovinae; Bos.

TITLE 1 (bases 1 to 356)

JOURNAL Sonstegard,T.S., Capuco,A.V., Van Tassel,J.C.P., Ashwell,M.S. and

COMMENT Mapping of Expressed Sequence Tags from a normalized bovine mammary

gland cDNA library

USDA, ARS, Beltsville Agricultural Research Center

Unpublished (2000)

Plasmid 200 Rm 2A, Beltsville, MD 20705, USA

Tel: 301 504 8416

Fax: 301 504 8414

Email: tads@psl.barc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred

v0.980904.e. Vector identified by cross-match with the -minscore 18

and -mismatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCTGCTGACGACG

Plate: 144 row: 1 column: 11

Seq primer: ATTGAGTACGCTATGAC

Location/Qualifiers

1..356

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone.lib="BARC 5BOV"

/tissue_type="pooled"

/lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;

Library made from pooled mRNA isolated from mammary

tissues at eight physiological, developmental, and disease

states"

BASE COUNT 70 a 118 c 94 g 74 t

ORIGIN

Query Match 17.9%; Score 84; DB 167; Length 356;

Best Local Similarity 66.7%; Pred. No. 7.1e-13;

Matches 120; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 232 ctaaactagagcagtgatgacatgagctctatctgtgtgcaaggaatcaagaagc 291

DB 2 CTGACGTTAGAGCGCGTGAACATCACTGACTGAAACAGGAGGAGGAGCGCG 61

QY 292 ttaaccttaccgagcgagatgaggtcaccctcagcttcgaagtcgagctcaccg 351

DB 62 TTGGCTTATATCCGCTTCACACAGGCGCCACACAGCTTGTGAGTCACGCTGCTCC 121

QY 352 ggcctgttcctgtgcaaggtgctgaagcagatcagcgttcgaagactcaagcagctcc 411

DB 122 GGCTGCTTCTCTGACATCACTGAGGCGGAGCCGCTGAGGCGCTGACCAATATGCCC 181

RESULT 13

LOCUS BE563442

DEFINITION BE563442 976 bp mRNA EST 15-AUG-2000

ACCESSION 601335496F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689710 5',

VERSION mRNA sequence.

KEYWORDS BE563442 GI:9607162

SOURCE EST.

ORGANISM human.

REFERENCE Homo sapiens

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

JOURNAL Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

CONTACT: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.L.Strausberg@nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM384 row: o column: 23

High quality sequence stop: 742.

Location/Qualifiers

1..976

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone.lib="IMAGE:3689710"

/tissue_type="pancreas"

/lab_host="DH10B (phage-resistant)"

/note="Organ: pancreas; Vector: pORF7; Site_1: XhoI;

Site_2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAGG. Library constructed

by Ling Hong in the laboratory of Gerald M. Rubin

(University of California, Berkeley) using ZAP-cDNA

synthesis kit (Stratagene) and Superscript II RT (Life

Technologies)."

BASE COUNT 241 a 231 c 298 g 206 t

ORIGIN

Query Match 14.3%; Score 66.8; DB 136; Length 976;

Best Local Similarity 53.7%; Pred. No. 5.1e-08;

Matches 216; Conservative 0; Mismatches 167; Indels 19; Gaps 3;

QY 24 ctccgaatgaagagctggcagctgacatgcttctcgtcataataaccagctttagc 83

DB 368 CTTCAGAAATCTGGAGTGTAAACAGAGACCTTCTATCTGAGAGAACACCACTAGTGC 427

QY 84 tgaagagctgcatgacgaggaagatcattaaagtggaagatcagctgtgtcccatg 143

DB 428 CGGATACCTTGCAAGACCAAAATGTCAATTTAGAGAAAGATGATGTACCCATTGA 487

QY 144 gtggctgagatgcaagcctgtcccccctacatcctgagtggtgcaggtggaagcagtgct 203

DB 488 GCGTCATGCTC-----TGTTCTTGGGAATCCATGAGGAGGAAGATGCGCT 532

QY 204 gtcattgtgggtg---ggcaggaagcagctataacatagagcagtgaaatcatgga 260

DB 533 GTCTCTGTCAAGTGTGATGATGAGACACAGACTCCAGCTGAGGAGGAGTTAAATCACTGA 592

QY 261 gctctatctgtgtccaaagatccaaagcttccactctcccgccgaggaatggggt 320

DB 593 CCGAGCGGAACAGAAACAGAGACAGCGCTTCCGCTTCAATCCGCTGAGACA-GTGGCC 651

QY 321 caactcagcttcgagtcgctgctaccgagctgtctcctgtgcaaggtgctgtaagc 380

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